

DAVI251.001APC\_sequence listing.TXT  
SEQUENCE LISTING

<110> Melbourne Health  
Jane, Stephen (US Only)  
Wilanowski, Tomasz (US only)  
Ting, Stephen (US only)

<120> MAMMALIAN GRAINYHEAD TRANSCRIPTION FACTORS

<130> DAVI251.001APC

<140> US 10/524,619

<141> 2005-02-09

<150> PCT/AU03/01006

<151> 2003-08-08

<150> US 60/402055

<151> 2002-08-09

<150> AU2002951579

<151> 2002-08-22

<160> 46

<170> PatentIn version 3.1

<210> 1

<211> 1881

<212> DNA

<213> human

<220>

<221> CDS

<222> (94)..(1323)

<400> 1

ataagagagg ccattctgaca gctccagata cgacagtcac tgtctccata gcaacgatgc 60

ctacccactc catcaagaca gaaaccacgc cac atg gct tcg ctg tgg gaa tcc 114  
Met Ala Ser Leu Trp Glu Ser  
1 5

ccc cag cag tgt atc atc ctg agc cca ctg agc ggg tgg tgg ttt tcg 162  
Pro Gln Gln Cys Ile Ile Leu Ser Pro Leu Ser Gly Trp Trp Phe Ser  
10 15 20

atc gga atc tca ata ctg acc agt tca gct ctg gtg ctc aag ccc caa 210  
Ile Gly Ile Ser Ile Leu Thr Ser Ser Ala Leu Val Leu Lys Pro Gln  
25 30 35

atg ctc aaa ggc gaa ctc cag act cga cct tct cag aga cct tca agg 258  
Met Leu Lys Gly Glu Leu Gln Thr Arg Pro Ser Gln Arg Pro Ser Arg  
40 45 50 55

aag gcg ttc agg agg aac aac ttt gaa tat acc cta gaa gct tca aaa 306  
Lys Ala Phe Arg Arg Asn Asn Phe Glu Tyr Thr Leu Glu Ala Ser Lys  
60 65 70

tca ctt cga cag aag cca gga gac agt acc atg acg tac ctg aac aaa 354  
Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr Tyr Leu Asn Lys  
75 80 85

## DAVI251.001APC\_sequence listing.TXT

ggc Gly	cag Gln	ttc Phe 90	tat Tyr	ccc Pro	atc Ile	acc Thr	ttg Leu 95	aag Lys	gag Glu	gtg Val	agc Ser 100	agc Ser	agt Ser	gaa Glu	gga Gly	402
atc Ile	cat His 105	cat His	ccc Pro	atc Ile	agc Ser	aaa Lys 110	gtt Val	cga Arg	agt Ser	gtg Val 115	atc Ile	atg Met	gtg Val	gtt Val	ttt Phe	450
gct Ala 120	gaa Glu	gac Asp	aaa Lys	agc Ser	aga Arg 125	gaa Glu	gat Asp	cag Gln	tta Leu	agg Arg 130	cat His	tgg Trp	aag Lys	tac Tyr	tgg Trp 135	498
cac His	tcc Ser	cgg Arg	cag Gln	cac His 140	acc Thr	gct Ala	aaa Lys	caa Gln	aga Arg 145	tgc Cys	att Ile	gac Asp	ata Ile	gct Ala 150	gac Asp	546
tat Tyr	aaa Lys	gaa Glu	agc Ser 155	ttc Phe	aac Asn	act Thr	atc Ile	agt Ser 160	aac Asn	atc Ile	gag Glu	gag Glu	att Ile 165	gcg Ala	tat Tyr	594
aac Asn	gcc Ala 170	att Ile	tcc Ser	ttc Phe	aca Thr	tgg Trp	gac Asp 175	atc Ile	aac Asn	gat Asp	gaa Glu	gca Ala 180	aag Lys	gtt Val	ttc Phe	642
atc Ile 185	tct Ser	gtg Val	aac Asn	tgc Cys	tta Leu	agc Ser 190	aca Thr	gat Asp	ttc Phe	tct Ser	tcc Ser 195	cag Gln	aag Lys	gga Gly	gtg Val	690
aag Lys 200	ggg Gly	ttg Leu	cct Pro	ctt Leu	aac Asn 205	att Ile	caa Gln	gtt Val	gat Asp	acc Thr 210	tat Tyr	agt Ser	tac Tyr	aac Asn	aac Asn 215	738
cgc Arg	agc Ser	aac Asn	aag Lys	cct Pro 220	gtg Val	cac His	cgg Arg	gcc Ala	tac Tyr 225	tgc Cys	cag Gln	atc Ile	aag Lys	gtc Val 230	ttc Phe	786
tgt Cys	gac Asp	aag Lys	gga Gly 235	gct Ala	gag Glu	cgg Arg	aaa Lys	atc Ile 240	agg Arg	gat Asp	gaa Glu	gaa Glu	cga Arg 245	aag Lys	caa Gln	834
agc Ser	aaa Lys	aga Arg 250	aaa Lys	gtt Val	tct Ser	gat Asp	gtt Val 255	aaa Lys	gtg Val	cca Pro	ctg Leu	ctt Leu 260	ccc Pro	tct Ser	cac His	882
aag Lys	cga Arg 265	atg Met	gat Asp	atc Ile	aca Thr	gtt Val 270	ttc Phe	aaa Lys	ccc Pro	ttc Phe	att Ile 275	gat Asp	ctc Leu	gat Asp	act Thr	930
cag Gln 280	cct Pro	gtc Val	ctc Leu	ttc Phe	att Ile 285	cct Pro	gac Asp	gtg Val	cac His	ttt Phe 290	gcc Ala	aac Asn	ttg Leu	cag Gln	cgg Arg 295	978
ggc Gly	act Thr	cat His	gtc Val	ctt Leu 300	ccc Pro	att Ile	gcc Ala	tct Ser	gaa Glu 305	gaa Glu	ttg Leu	gag Glu	ggt Gly	gaa Glu 310	ggc Gly	1026
tct Ser	gtc Val	ttg Leu	aaa Lys 315	agg Arg	ggg Gly	ccg Pro	tac Tyr	ggc Gly 320	aca Thr	gaa Glu	gat Asp	gac Asp	ttt Phe 325	gct Ala	gtc Val	1074
cct Pro	cct Pro	tct Ser	acc Thr	aag Lys	ctg Leu	gcc Ala	cgg Arg	ata Ile	gaa Glu	gaa Glu	cca Pro	aag Lys	aga Arg	gtg Val	ctg Leu	1122

## DAVI251.001APC\_sequence listing.TXT

```

330                                     335                                     340
ctc tac gtt cga aag gag tca gaa gaa gtc ttt gat gcc ctg atg ctc      1170
Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu Met Leu
345                                     350                                     355

aaa acc cca tct ttg aag ggc ttg atg gaa gct atc tca gac aaa tac      1218
Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp Lys Tyr
360                                     365                                     370                                     375

gat gtt ccc cat gac aag att ggg aaa ata ttc aag aag tgt aaa aag      1266
Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys Lys Lys
380                                     385                                     390

ggg atc ctg gtg aac atg gac gac aac att gtg aag cat tac tcc aat      1314
Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr Ser Asn
395                                     400                                     405

gag gac acc ttccagctgc agattgaaga agccgggggg tcttacaagc      1363
Glu Asp Thr
410

tcaccctgac ggagatctaa aggcctgctg gccacagctc cccaggagtt cagtgcaggt      1423

gtttctagat cttacggttt ggcaactgca ggtaacccca gtcagccatg tcgccagcac      1483

aggtctatgt cgagggaatg ggttccttgc aggttgagg cggggctgca tctggcttgg      1543

tggtagcatt taatctattg cattggtgtt ttccagatga aagagaaatc catataccat      1603

tatgtttgaa tttcctgata tatacaggat ttaaagtgaa aactttattc caagagttaa      1663

cagagtctct gggaagcttt aggacatctg ctacgttatt tatcaaaata ttgggatctc      1723

tgccttgctg ctacagtgtc gtgggcctgc tcgctagcag aagtcagaaa aggcgatagg      1783

cttggttta aggatttcgt gcccttgctc gaattcagta caactccact gcctcacgtt      1843

agcgggagcg cacctgaaga gtacgggggg agccctct      1881

<210> 2
<211> 410
<212> PRT
<213> human

<400> 2
Met Ala Ser Leu Trp Glu Ser Pro Gln Gln Cys Ile Ile Leu Ser Pro
1 5 10 15

Leu Ser Gly Trp Trp Phe Ser Ile Gly Ile Ser Ile Leu Thr Ser Ser
20 25 30

Ala Leu Val Leu Lys Pro Gln Met Leu Lys Gly Glu Leu Gln Thr Arg
35 40 45

Pro Ser Gln Arg Pro Ser Arg Lys Ala Phe Arg Arg Asn Asn Phe Glu
50 55 60

```

DAVI251.001APC\_sequence listing.TXT

Tyr Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser  
 65 70 75 80  
 Thr Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys  
 85 90 95  
 Glu Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg  
 100 105 110  
 Ser val Ile Met val val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln  
 115 120 125  
 Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln  
 130 135 140  
 Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser  
 145 150 155 160  
 Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile  
 165 170 175  
 Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp  
 180 185 190  
 Phe Ser Ser Gln Lys Gly val Lys Gly Leu Pro Leu Asn Ile Gln val  
 195 200 205  
 Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala  
 210 215 220  
 Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile  
 225 230 235 240  
 Arg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp val Lys  
 245 250 255  
 Val Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys  
 260 265 270  
 Pro Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp val  
 275 280 285  
 His Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser  
 290 295 300  
 Glu Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly  
 305 310 315 320

DAVI251.001APC\_sequence listing.TXT

Thr Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile  
325 330 335

Glu Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu  
340 345 350

Val Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met  
355 360 365

Glu Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys  
370 375 380

Ile Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn  
385 390 395 400

Ile Val Lys His Tyr Ser Asn Glu Asp Thr  
405 410

<210> 3  
<211> 2361  
<212> DNA  
<213> human

<220>  
<221> CDS  
<222> (7)..(1860)

<220>  
<221> VARIANT  
<222> 342  
<223> Xaa = Lys, Ile

<400> 3	
agcgcg atg aca cag gag tac gac aac aaa cgg cca gtg ttg gtt ctt	48
Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu	
1 5 10	
cag aat gaa gca ctt tat cca cag cgg cgg tcc tac act agt gag gat	96
Gln Asn Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp	
15 20 25 30	
gag gcc tgg aaa tcc ttc ctg gaa aac cct ctc act gca gcg acc aaa	144
Glu Ala Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys	
35 40 45	
gcg atg atg agc atc aat gga gat gaa gac agc gcc gct gcg ctg ggc	192
Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Leu Gly	
50 55 60	
ctg ctc tat gac tac tac aag gtt cca aga gag aga agg tca tca aca	240
Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Ser Ser Thr	
65 70 75	
gca aag cca gag gtg gag cac cct gag cca gat cac agc aaa aga aac	288

## DAVI251.001APC\_sequence listing.TXT

Ala	Lys	Pro	Glu	Val	Glu	His	Pro	Glu	Pro	Asp	His	Ser	Lys	Arg	Asn	
80					85					90						
agc	ata	cca	att	gtg	aca	gag	cag	ccc	ctc	atc	tct	gct	gga	gaa	aac	336
Ser	Ile	Pro	Ile	Val	Thr	Glu	Gln	Pro	Leu	Ile	Ser	Ala	Gly	Glu	Asn	110
95					100					105						
aga	gtg	caa	gta	ctg	aaa	aat	gtg	cca	ttt	aac	att	gtc	ctt	ccc	cat	384
Arg	Val	Gln	Val	Leu	Lys	Asn	Val	Pro	Phe	Asn	Ile	Val	Leu	Pro	His	125
				115					120					125		
ggc	aac	cag	ctg	ggc	att	gat	aag	aga	ggc	cat	ctg	aca	gct	tca	gat	432
Gly	Asn	Gln	Leu	Gly	Ile	Asp	Lys	Arg	Gly	His	Leu	Thr	Ala	Ser	Asp	140
			130					135					140			
acg	aca	gtc	act	gtc	tcc	ata	gca	acg	atg	cct	acc	cac	tcc	atc	aag	480
Thr	Thr	Val	Thr	Val	Ser	Ile	Ala	Thr	Met	Pro	Thr	His	Ser	Ile	Lys	155
		145					150					155				
aca	gaa	acc	cag	cca	cat	ggc	ttc	gct	gtg	gga	atc	ccc	cca	gca	gtg	528
Thr	Glu	Thr	Gln	Pro	His	Gly	Phe	Ala	Val	Gly	Ile	Pro	Pro	Ala	Val	170
	160					165					170					
tat	cat	cct	gag	ccc	act	gag	cgg	gtg	gtg	gtt	ttc	gat	cgg	aay	ctc	576
Tyr	His	Pro	Glu	Pro	Thr	Glu	Arg	Val	Val	Val	Phe	Asp	Arg	Asn	Leu	190
					180					185						
aat	act	gac	cag	ttc	agc	tct	ggt	gct	caa	gcc	cca	aat	gct	caa	agg	624
Asn	Thr	Asp	Gln	Phe	Ser	Ser	Gly	Ala	Gln	Ala	Pro	Asn	Ala	Gln	Arg	205
				195					200					205		
cga	act	cca	gac	tcg	acc	ttc	tca	gag	acc	ttc	aag	gaa	ggc	gtt	cag	672
Arg	Thr	Pro	Asp	Ser	Thr	Phe	Ser	Glu	Thr	Phe	Lys	Glu	Gly	Val	Gln	220
			210					215					220			
gag	gtt	ttc	ttc	ccc	tcg	gat	ctc	agt	ctg	cgg	atg	cct	ggc	atg	aat	720
Glu	Val	Phe	Phe	Pro	Ser	Asp	Leu	Ser	Leu	Arg	Met	Pro	Gly	Met	Asn	235
		225					230					235				
tca	gag	gac	tat	gtt	ttt	gac	agt	gtt	tct	ggg	aac	aac	ttt	gaa	tat	768
Ser	Glu	Asp	Tyr	Val	Phe	Asp	Ser	Val	Ser	Gly	Asn	Asn	Phe	Glu	Tyr	250
	240					245					250					
acc	cta	gaa	gct	tca	aaa	tca	ctt	cga	cag	aag	cca	gga	gac	agt	acc	816
Thr	Leu	Glu	Ala	Ser	Lys	Ser	Leu	Arg	Gln	Lys	Pro	Gly	Asp	Ser	Thr	270
					260					265						
atg	acg	tac	ctg	aac	aaa	ggc	cag	ttc	tat	ccc	atc	acc	ttg	aag	gag	864
Met	Thr	Tyr	Leu	Asn	Lys	Gly	Gln	Phe	Tyr	Pro	Ile	Thr	Leu	Lys	Glu	285
				275					280					285		
gtg	agc	agc	agt	gaa	gga	atc	cat	cat	ccc	atc	agc	aaa	gtt	cga	agt	912
Val	Ser	Ser	Ser	Glu	Gly	Ile	His	His	Pro	Ile	Ser	Lys	Val	Arg	Ser	300
			290					295					300			
gtg	atc	atg	gtg	gtt	ttt	gct	gaa	gac	aaa	agc	aga	gaa	gat	cag	tta	960
Val	Ile	Met	Val	Val	Phe	Ala	Glu	Asp	Lys	Ser	Arg	Glu	Asp	Gln	Leu	315
		305					310					315				
agg	cat	tgg	aag	tac	tgg	cac	tcc	cgg	cag	cac	acc	gct	aaa	caa	aga	1008
Arg	His	Trp	Lys	Tyr	Trp	His	Ser	Arg	Gln	His	Thr	Ala	Lys	Gln	Arg	330
	320					325					330					

DAVI251.001APC\_sequence\_listing.TXT

tgc att gac ata gct gac tat awa gaa agc ttc aac act atc agt aac Cys Ile Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn 335 340 345 350	1056
atc gag gag att gcg tat aac gcc att tcc ttc aca tgg gac atc aac Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn 355 360 365	1104
gat gaa gca aag gtt ttc atc tct gtg aac tgc tta agc aca gat ttc Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe 370 375 380	1152
tct tcc cag aag gga gtg aag ggg ttg cct ctt aac att caa gtt gat Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp 385 390 395	1200
acc tat agt tac aac aac cgc agc aac aag cct gtg cac cgg gcc tac Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr 400 405 410	1248
tgc cag atc aag gtc ttc tgt gac aag gga gct gag cgg aaa atc agg Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg 415 420 425 430	1296
gat gaa gaa cga aag caa agc aaa aga aaa gtt tct gat gtt aaa gtg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val 435 440 445	1344
cca ctg ctt ccc tct cac aag cga atg gat atc aca gtt ttc aaa ccc Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro 450 455 460	1392
ttc att gat ctc gat act cag cct gtc ctc ttc att cct gac gtg cac Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His 465 470 475	1440
ttt gcc aac ttg cag cgg ggc act cat gtc ctt ccc att gcc tct gaa Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser Glu 480 485 490	1488
gaa ttg gag ggt gaa ggc tct gtc ttg aaa agg ggg ccg tac ggc aca Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr 495 500 505 510	1536
gaa gat gac ttt gct gtc cct cct tct acc aag ctg gcc cgg ata gaa Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu 515 520 525	1584
gaa cca aag aga gtg ctg ctc tac gtt cga aag gag tca gaa gaa gtc Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val 530 535 540	1632
ttt gat gcc ctg atg ctc aaa acc cca tct ttg aag ggc ttg atg gaa Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu 545 550 555	1680
gct atc tca gac aaa tac gat gtt ccc cat gac aag att ggg aaa ata Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile 560 565 570	1728
ttc aag aag tgt aaa aag ggg atc ctg gtg aac atg gac gac aac att Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile 575 580 585 590	1776

DAVI251.001APC\_sequence listing.TXT

```

gtg aag cat tac tcc aat gag gac acc ttc cag ctg cag att gaa gaa      1824
Val Lys His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu
                    595                      600                      605

gcc ggg ggg tct tac aag ctc acc ctg acg gag atc taaaggcctg      1870
Ala Gly Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
                    610                      615

cggggccacag ctccccagga gttcagtgca ggtgttttcta gatcttacgg tttggcaact      1930
gcaggttaacc ccagtcagcc atgtcgccag cacaggtcta tgtcgagggga atgggttcct      1990
tgcaggtttg aggcggggct gcatctggct tggtagtagc atttaatcta ttgcattggt      2050
gtttttcaga tgaaagagaa atccatatac cattatgttt gaatttcctg atatatacag      2110
gatttaaagt gaaaacttta ttccaagagt taacagagtc tctgggaagc tttaggacat      2170
ctgctacgtt atttatcaaa atattgggat ctctgccttg tgcctacagt gtcgtgggcc      2230
tgctcgctag cagaagtcag aaaaggcgat aggcttggt ttaaggattt cgtgcccttg      2290
cctgaattca gtacaactcc actgcctcac gttagcggga gcgcacctga agagtacggg      2350
gggagccctc t                                                    2361

```

<210> 4  
 <211> 618  
 <212> PRT  
 <213> human

<220>  
 <221> misc\_feature  
 <222> (342)..(342)  
 <223> The 'Xaa' at location 342 stands for Lys, or Ile.

<400> 4

```

Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu Gln Asn
1          5          10          15

```

```

Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp Glu Ala
          20          25          30

```

```

Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
          35          40          45

```

```

Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly Leu Leu
          50          55          60

```

```

Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr Ala Lys
65          70          75          80

```

```

Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn Ser Ile
          85          90          95

```



DAVI251.001APC\_sequence listing.TXT

Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val  
100 105 110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Gly Asn  
115 120 125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp Thr Thr  
130 135 140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu  
145 150 155 160

Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His  
165 170 175

Pro Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Asn Leu Asn Thr  
180 185 190

Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg Arg Thr  
195 200 205

Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val  
210 215 220

Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu  
225 230 235 240

Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu  
245 250 255

Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr  
260 265 270

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser  
275 280 285

Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile  
290 295 300

Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His  
305 310 315 320

Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile  
325 330 335

Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu  
340 345 350

DAVI251.001APC\_sequence listing.TXT

Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu  
 355 360 365  
 Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser  
 370 375 380  
 Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr  
 385 390 395 400  
 Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln  
 405 410 415  
 Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu  
 420 425 430  
 Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu  
 435 440 445  
 Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile  
 450 455 460  
 Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala  
 465 470 475 480  
 Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu  
 485 490 495  
 Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp  
 500 505 510  
 Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro  
 515 520 525  
 Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp  
 530 535 540  
 Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile  
 545 550 555 560  
 Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys  
 565 570 575  
 Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys  
 580 585 590  
 His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly

DAVI251.001APC\_sequence listing.TXT

595

600

605

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile  
610 615

<210> 5  
<211> 4532  
<212> DNA  
<213> human

<220>  
<221> CDS  
<222> (67)..(1941)

<400> 5  
ttgaaagtcc agtttcacca gaggctgagg ctccaggaaa aggggagcaa gttcattgga 60  
tcaaac atg tca caa gag tca gac aat aat aaa aga cta gtg gcc tta 108  
Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu  
1 5 10  
gtg ccc atg ccc agt gac cct cca ttc aat acc cga aga gcc tac acc 156  
Val Pro Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr  
15 20 25 30  
agt gag gat gaa gcc tgg aag tca tac ttg gag aat ccc ctg aca gca 204  
Ser Glu Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala  
35 40 45  
gcc acc aag gcc atg atg agc att aat ggt gat gag gac agt gct gct 252  
Ala Thr Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala  
50 55 60  
gcc ctc ggc ctg ctc tat gac tac tac aag gtt cct cga gac aag agg 300  
Ala Leu Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg  
65 70 75  
ctg ctg tct gta agc aaa gca agt gac agc caa gaa gac cag gag aaa 348  
Leu Leu Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys  
80 85 90  
aga aac tgc ctt ggc acc agt gaa gcc cag agt aat ttg agt gga gga 396  
Arg Asn Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly  
95 100 105 110  
gaa aac cga gtg caa gtc cta aag act gtt cca gtg aac ctt tcc cta 444  
Glu Asn Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu  
115 120 125  
aat caa gat cac ctg gag aat tcc aag cgg gaa cag tac agc atc agc 492  
Asn Gln Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser  
130 135 140  
ttc ccc gag agc tct gcc atc atc ccg gtg tcg gga atc acg gtg gtg 540  
Phe Pro Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val  
145 150 155  
aaa gct gaa gat ttc aca cca gtt ttc atg gcc cca cct gtg cac tat 588  
Lys Ala Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr  
160 165 170

## DAVI251.001APC\_sequence listing.TXT

ccc Pro 175	cgg Arg	gga Gly	gat Asp	ggg Gly	gaa Glu 180	gag Glu	caa Gln	cga Arg	gtg Val 185	gtt Val 185	atc Ile	ttt Phe	gaa Glu	cag Gln	act Thr 190	636
cag Gln	tat Tyr	gac Asp	gtg Val	ccc Pro 195	tcg Ser	ctg Leu	gcc Ala	acc Thr	cac His 200	agc Ser	gcc Ala	tat Tyr	ctc Leu	aaa Lys 205	gac Asp	684
gac Asp	cag Gln	cgc Arg	agc Ser 210	act Thr	ccg Pro	gac Asp	agc Ser	aca Thr 215	tac Tyr	agc Ser	gag Glu	agc Ser	ttc Phe 220	aag Lys	gac Asp	732
gca Ala	gcc Ala	aca Thr 225	gag Glu	aaa Lys	ttt Phe	cgg Arg	agt Ser 230	gct Ala	tca Ser	gtt Val	ggg Gly 235	gct Ala	gag Glu	gag Glu	tac Tyr	780
atg Met 240	tat Tyr	gat Asp	cag Gln	aca Thr	tca Ser	agt Ser 245	ggc Gly	aca Thr	ttt Phe	cag Gln	tac Tyr 250	acc Thr	ctg Leu	gaa Glu	gcc Ala	828
acc Thr 255	aaa Lys	tct Ser	ctc Leu	cgt Arg	cag Gln 260	aag Lys	cag Gln	ggg Gly	gag Glu	ggc Gly 265	ccc Pro	atg Met	acc Thr	tac Tyr	ctc Leu 270	876
aac Asn	aaa Lys	gga Gly	cag Gln	ttc Phe 275	tat Tyr	gcc Ala	ata Ile	aca Thr	ctc Leu 280	agc Ser	gag Glu	acc Thr	gga Gly	gac Asp 285	aac Asn	924
aaa Lys	tgc Cys	ttc Phe	cga Arg 290	cac His	ccc Pro	atc Ile	agc Ser	aaa Lys 295	gtc Val	agg Arg	agt Ser	gtg Val 300	gtg Val 300	atg Met	gtg Val	972
gtc Val	ttc Phe	agt Ser 305	gaa Glu	gac Asp	aaa Lys	aac Asn	aga Arg 310	gat Asp	gaa Glu	cag Gln	ctc Leu	aaa Lys 315	tac Tyr	tgg Trp	aaa Lys	1020
tac Tyr 320	tgg Trp	cac His	tct Ser	cgg Arg	cag Gln	cat His 325	acg Thr	gcg Ala	aag Lys	cag Gln	agg Arg 330	gtc Val	ctt Leu	gac Asp	att Ile	1068
gcc Ala 335	gat Asp	tac Tyr	aag Lys	gag Glu	agc Ser 340	ttt Phe	aat Asn	acg Thr	att Ile	gga Gly 345	aac Asn	att Ile	gaa Glu	gag Glu	att Ile 350	1116
gca Ala	tat Tyr	aat Asn	gct Ala 355	gtt Val	tcc Ser	ttt Phe	acc Thr	tgg Trp	gac Asp 360	gtg Val	aat Asn	gaa Glu	gag Glu	gcg Ala 365	aag Lys	1164
att Ile	ttc Phe	atc Ile	acc Thr 370	gtg Val	aat Asn	tgc Cys	ttg Leu	agc Ser 375	aca Thr	gat Asp	ttc Phe	tcc Ser	tcc Ser	caa Gln	aaa Lys	1212
ggg Gly	gtg Val	aaa Lys 385	gga Gly	ctt Leu	cct Pro	ttg Leu	atg Met 390	att Ile	cag Gln	att Ile	gac Asp	aca Thr 395	tac Tyr	agt Ser	tat Tyr	1260
aac Asn 400	aat Asn	cgt Arg	agc Ser	aat Asn	aaa Lys	ccc Pro 405	att Ile	cat His	aga Arg	gct Ala	tat Tyr 410	tgc Cys	cag Gln	atc Ile	aag Lys	1308
gtc Val	ttc Phe	tgt Cys	gac Asp	aaa Lys	gga Gly	gca Ala	gaa Glu	aga Arg	aaa Lys	atc Ile	cga Arg	gat Asp	gaa Glu	gag Glu	cgg Arg	1356

DAVI251.001APC\_sequence listing.TXT

415	420	425	430	
aag cag aac agg aag aaa ggg aaa ggc cag gcc tcc caa act caa tgc	Lys Gln Asn Arg Lys 435	Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys	1404	
aac agc tcc tct gat ggg aag ttg gct gcc ata cct tta cag aag aag	Asn Ser Ser Ser Asp 450	Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys	1452	
agt gac atc acc tac ttc aaa acc atg cct gat ctc cac tca cag cca	Ser Asp Ile Thr Tyr Phe Lys 470	Thr Met Pro Asp Leu His Ser Gln Pro	1500	
gtt ctc ttc ata cct gat gtt cac ttt gca aac ctg cag agg acc gga	Val Leu Phe Ile Pro Asp Val 485	His Phe Ala Asn Leu Gln Arg Thr Gly	1548	
cag gtg tat tac aac acg gat gat gaa cga gaa ggt ggc agt gtc ctt	Gln Val Tyr Tyr Asn Thr 500	Asp Asp Glu Arg Glu Gly Ser Val Leu	1596	
gtt aaa cgg atg ttc cgg ccc atg gaa gag gag ttt ggt cca gtg cct	Val Lys Arg Met Phe 515	Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro	1644	
tca aag cag atg aaa gaa gaa ggg aca aag cga gtg ctc ttg tac gtg	Ser Lys Gln Met Lys 530	Glu Glu Gly Thr Lys Arg Val Leu Tyr Val	1692	
agg aag gag act gac gat gtg ttc gat gca ttg atg ttg aag tct ccc	Arg Lys Glu Thr Asp Asp Val 550	Asp Ala Leu Met Leu Lys Ser Pro	1740	
aca gtg aag ggc ctg atg gaa gcg ata tct gag aaa tat ggg ctg ccc	Thr Val Lys Gly Leu Met Glu 565	Ala Ile Ser Glu Lys Tyr Gly Leu Pro	1788	
gtg gag aag ata gca aag ctt tac aag aaa agc aaa aaa ggc atc ttg	Val Glu Lys Ile Ala Lys 580	Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu	1836	
gtg aac atg gat gac aac atc atc gag cac tac tcg aac gag gac acc	Val Asn Met Asp Asp Asn Ile Ile Glu 600	His Tyr Ser Asn Glu Asp Thr	1884	
ttc atc ctc aac atg gag agc atg gtg gag ggc ttc aag gtc acg ctc	Phe Ile Leu Asn Met Glu Ser Met Val 615	Glu Gly Phe Lys Val Thr Leu	1932	
atg gaa atc tagccctggg tttggcatcc gctttggctg gagctctcag	Met Glu Ile 625		1981	
tgcgttcctc cctgagagag acagaagccc cagccccaga acctggagac ccattctcccc			2041	
catctcaciaa ctgctgttac aagaccgtgc tggggagtg ggcaagggac aggccccact			2101	
gtcgggtgtgc ttggcccatc cactggcacc taccacggag ctgaagcctg agcccctcag			2161	
gaaggtgcct taggcctgtt ggattcctat ttattgccca ccttttcctg gagcccaggt			2221	
ccaggccccgc caggactctg caggtcactg ctagctccag atgagaccgt ccagcgttcc			2281	

## DAVI251.001APC\_sequence listing.TXT

cccttcaaga gaaacactca tcccgaacag ctaaaaaaat tcccatccct tctctctcac	2341
ccctccatat ctatctcccg agtggctgga caaaatgagc tacgtctggg tgcagtagtt	2401
ataggtgggg caagaggtgg atgcccactt tctggtcaga cacctttagg ttgctctggg	2461
gaaggctgtc ttgctaaata cctccagggg tcccagcaag tggccaccag gccttgtaca	2521
ggaagacatt cagtcaccgt gtaattagta acacagaaag tctgcctgtc tgcattgtac	2581
atagtgttta taatattgta ataatatatt ttacctgtgg tatgtgggca tgtttactgc	2641
cactggcctt agaggagaca cagacctgga gaccgtttta atggggggtt ttgcctctgt	2701
gcctgttcaa gagacttgca gggctaggta gagggccttt gggatgttaa ggtgactgca	2761
gctgatgcca agatggactc tgcaatgggc atacctgggg gctcgttccc tgtccccaga	2821
ggaagcccc tctccttctc catgggcatg actctccttc gaggccacca cgtttatctc	2881
acaatgatgt gttttgcttg actttccctt tgcgctgtct cgtgggaaag gtcattctgt	2941
ctgagacccc agctccttct ccagctttgg ctgcgggcat ggcctgagct ttctggagag	3001
cctctgcagg gggtttgcca tcagggccct gtggctgggt ctgctgcaga gctccttggc	3061
tatcaggaga atcctggaca ctgtactgtg cctcccagtt taaaaacacg cccttcatct	3121
caagtggccc tttaaaaggc ctgctgccat gtgagagctg tgaacagctc agctctgagt	3181
cggcaggctg gggcttcctc ctgggccacc agatggaaag ggggtattgt ttgcctcact	3241
cctggatgct gcgttttaag gaagtgagtg agaaagaatg tgccaagata cctggctcct	3301
gtgaaaccag cctcaggagg gaaactggga gagagaagct gtggtctcct gctacatgcc	3361
ctgggagctg gaagagaaaa aactcccct aaacaatcgc aaaatgatga accatcatgg	3421
gccactgttc tctttgaggg gacaggttta ggggtttgcg ttcgcccttg tgggctgaag	3481
cactagcttt ttggtagcta gacacatcct gcacccaaag gttctctaca aaggcccaga	3541
tttgtttgta aagcactttg actcttacct ggaggccgc tctctaaggg cttcctgcgc	3601
tcccacctca tctgtccctg agatgcagag caggatggag ggtctgcttc tagctcagct	3661
gtttctcctt gaggttgcgg aggaattgaa ttgaatggga cagagggcag gtgctgtggc	3721
caagaagatc tccgagcagc agtgacgggg caccttgctg tgtgtcctct gggcatgtta	3781
acccttctgt ggggccaaag gtttgcatcg tggatccagc tgtgctccag tctgtcccct	3841
cctcctccac tctgactgcc acgccccgga ccagcagctt ggggaccctc cagggtacta	3901
atggggctct gttctgagat ggacaaattc agtgttggaa atacatgttg tactatgcac	3961
ttcccatgct cctagggtta ggaatagttt caaacatgat tggcagacat aacaacggca	4021
aatactcgga ctggggcata ggactccaga gtaggaaaaa gacaaaagat ttggcagcct	4081
gacacaggca acctaccct ctctctccag cctctttatg aaactgtttg tttgccagtc	4141

DAVI251.001APC\_sequence listing.TXT

```

ctgccctaag gcagaagatg aattgaagat gctgtgcatg tttcctaagt ccttgagcaa 4201
tcatggtggt gacaattgcc acaagggata tgaggccagt gccaccagag ggtggtgcca 4261
agtgccacat cccttccgat ccattcccct ctgcatcctc ggagcacccc agtttgcctt 4321
tgatgtgtcc gctgtgtatg ttagctgaac tttgatgagc aaaatttcct gagcgaaaca 4381
ctccaaagag ataggaaaac ttgccgcctc ttcttttttg tcccttaatc aaactcaaat 4441
aagcttaaaa aaaatccatg gaagatcatg gacatgtgaa atgagcattt ttttcttttt 4501
tttttttttt tttaacaaag tctgaactga g 4532

```

<210> 6  
 <211> 625  
 <212> PRT  
 <213> human

<400> 6

Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro  
 1 5 10 15

Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu  
 20 25 30

Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr  
 35 40 45

Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu  
 50 55 60

Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu  
 65 70 75 80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys Arg Asn  
 85 90 95

Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly Glu Asn  
 100 105 110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu Asn Gln  
 115 120 125

Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser Phe Pro  
 130 135 140

Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala  
 145 150 155 160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg

DAVI251.001APC\_sequence listing.TXT  
165 170 175

Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr  
180 185 190

Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp Asp Gln  
195 200 205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Ala Ala  
210 215 220

Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr Met Tyr  
225 230 235 240

Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys  
245 250 255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys  
260 265 270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys  
275 280 285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe  
290 295 300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp  
305 310 315 320

His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp  
325 330 335

Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr  
340 345 350

Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe  
355 360 365

Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val  
370 375 380

Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn  
385 390 395 400

Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe  
405 410 415



DAVI251.001APC\_sequence listing.TXT

Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln  
420 425 430

Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys Asn Ser  
435 440 445

Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp  
450 455 460

Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu  
465 470 475 480

Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val  
485 490 495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu Val Lys  
500 505 510

Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro Ser Lys  
515 520 525

Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val Arg Lys  
530 535 540

Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val  
545 550 555 560

Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro Val Glu  
565 570 575

Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn  
580 585 590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile  
595 600 605

Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu Met Glu  
610 615 620

Ile  
625

<210> 7  
<211> 1870  
<212> DNA  
<213> HUMAN

<220>  
<221> CDS

## DAVI251.001APC\_sequence listing.TXT

&lt;222&gt; (47)..(1867)

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 117

&lt;223&gt; Xaa = Phe, Leu

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 172

&lt;223&gt; Xaa = Thr

&lt;400&gt; 7

aggagatgtg ccaaactggt aagagtggtt atttctgagc agaaga atg tgg atg 55  
 Met Trp Met  
 1

aat tcc att ctt cct att ttt ctt ttc agg tct gtg cgg ctg cta aag 103  
 Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg Leu Leu Lys  
 5 10 15

aac gac cca gtc aac ttg cag aaa ttc tct tac act agt gag gat gag 151  
 Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser Glu Asp Glu  
 20 25 30 35

gcc tgg aag acg tac cta gaa aac ccg ttg aca gct gcc aca aag gcc 199  
 Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala  
 40 45 50

atg atg aga gtc aat gga gat gat gac agt gtt gcg gcc ttg agc ttc 247  
 Met Met Arg Val Asn Gly Asp Asp Asp Ser Val Ala Ala Leu Ser Phe  
 55 60 65

ctc tat gat tac tac atg ggt ccc aag gag aag cgg ata ttg tcc tcc 295  
 Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser  
 70 75 80

agc act ggg ggc agg aat gac caa gga aag agg tac tac cat ggc atg 343  
 Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr His Gly Met  
 85 90 95

gaa tat gag acg gac ctc act ccc ctt gaa agc ccc aca cac ctc atg 391  
 Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr His Leu Met  
 100 105 110 115

aaa ytc ctg aca gag aac gtg tct gga acc cca gag tac cca gat ttg 439  
 Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr Pro Asp Leu  
 120 125 130

ctc aag aag aat aac ctg atg agc ttg gag ggg gcc ttg ccc acc cct 487  
 Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu Pro Thr Pro  
 135 140 145

ggc aag gca gct ccc ctc cct gca ggc ccc agc aag ctg gag gcc ggc 535  
 Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu Glu Ala Gly  
 150 155 160

tct gtg gac agc tac ctg tta ccc acy act gat atg tat gat aat ggc 583  
 Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr Asp Asn Gly  
 165 170 175

## DAVI251.001APC\_sequence listing.TXT

tcc Ser 180	ctc Leu	aac Asn	tcc Ser	ttg Leu	ttt Phe 185	gag Glu	agc Ser	att Ile	cat His	ggg Gly 190	gtg Val	ccg Pro	ccc Pro	aca Thr	cag Gln 195	631
cgc Arg	tgg Trp	cag Gln	cca Pro	gac Asp 200	agc Ser	acc Thr	ttc Phe	aaa Lys	gat Asp 205	gac Asp	cca Pro	cag Gln	gag Glu	tcg Ser 210	atg Met	679
ctc Leu	ttc Phe	cca Pro	gat Asp 215	atc Ile	ctg Leu	aaa Lys	acc Thr	tcc Ser 220	ccg Pro	gaa Glu	ccc Pro	cca Pro	tgt Cys 225	cca Pro	gag Glu	727
gac Asp	tac Tyr	ccc Pro 230	agc Ser	ctc Leu	aaa Lys	agt Ser	gac Asp 235	ttt Phe	gaa Glu	tac Tyr	acc Thr	ctg Leu 240	ggc Gly	tcc Ser	ccc Pro	775
aaa Lys	gcc Ala 245	atc Ile	cac His	atc Ile	aag Lys	tca Ser 250	ggc Gly	gag Glu	tca Ser	ccc Pro	atg Met 255	gcc Ala	tac Tyr	ctc Leu	aac Asn	823
aaa Lys 260	ggc Gly	cag Gln	ttc Phe	tac Tyr	ccc Pro 265	gtc Val	acc Thr	ctg Leu	cgg Arg	acc Thr 270	cca Pro	gca Ala	ggc Gly	ggc Gly	aaa Lys 275	871
ggc Gly	ctt Leu	gcc Ala	ttg Leu	tcc Ser 280	tcc Ser	aac Asn	aaa Lys	gtc Val	aag Lys 285	agt Ser	gtg Val	gtg Val	atg Met	gtt Val 290	gtc Val	919
ttc Phe	gac Asp	aat Asn	gag Glu 295	aag Lys	gtc Val	cca Pro	gta Val	gag Glu 300	cag Gln	ctg Leu	cgc Arg	ttc Phe	tgg Trp 305	aag Lys	cac His	967
tgg Trp	cat His	tcc Ser 310	cgg Arg	caa Gln	ccc Pro	act Thr	gcc Ala 315	aag Lys	cag Gln	cgg Arg	gtc Val	att Ile 320	gac Asp	gtg Val	gct Ala	1015
gac Asp	tgc Cys 325	aaa Lys	gaa Glu	aac Asn	ttc Phe	aac Asn 330	act Thr	gtg Val	gag Glu	cac His	att Ile 335	gag Glu	gag Glu	gtg Val	gcc Ala	1063
tat Tyr 340	aat Asn	gca Ala	ctg Leu	tcc Ser	ttt Phe 345	gtg Val	tgg Trp	aac Asn	gtg Val 350	aat Asn	gaa Glu	gag Glu	gcc Ala	aag Lys	gtg Val 355	1111
ttc Phe	atc Ile	ggc Gly	gta Val	aac Asn 360	tgt Cys	ctg Leu	agc Ser	aca Thr	gac Asp 365	ttt Phe	tcc Ser	tca Ser	caa Gln	aag Lys 370	ggg Gly	1159
gtg Val	aag Lys	ggc Gly	gtc Val 375	ccc Pro	ctg Leu	aac Asn	ctg Leu	cag Gln 380	att Ile	gac Asp	acc Thr	tat Tyr	gac Asp 385	tgt Cys	ggc Gly	1207
ttg Leu	ggc Gly	act Thr 390	gag Glu	cgc Arg	ctg Leu	gta Val	cac His 395	cgt Arg	gct Ala	gtc Val	tgc Cys	cag Gln 400	atc Ile	aag Lys	atc Ile	1255
ttc Phe	tgt Cys 405	gac Asp	aag Lys	gga Gly	gct Ala	gag Glu 410	agg Arg	aag Lys	atg Met	cgc Arg	gat Asp 415	gac Asp	gag Glu	cgg Arg	aag Lys	1303
cag Gln	ttc Phe	cgg Arg	agg Arg	aag Lys	gtc Val	aag Lys	tgc Cys	cct Pro	gac Asp	tcc Ser	agc Ser	aac Asn	agt Ser	ggc Gly	gtc Val	1351

DAVI251.001APC\_sequence listing.TXT

420	425	430	435	
aag ggc tgc ctg ctg tcg ggc ttc agg ggc aat gag acg acc tac ctt				1399
Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu	440	445	450	
cgg cca gag act gac ctg gag acg cca ccc gtg ctg ttc atc ccc aat				1447
Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe Ile Pro Asn	455	460	465	
gtg cac ttc tcc agc ctg cag cgc tct gga ggg gca gcc ccc tcg gca				1495
Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala Pro Ser Ala	470	475	480	
gga ccc agc agc tcc aac agg ctg cct ctg aag cgt acc tgc tcg ccc				1543
Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro	485	490	495	
ttc act gag gag ttt gag cct ctg ccc tcc aag cag gcc aag gaa ggc				1591
Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Gly	500	505	510	515
gac ctt cag aga gtt ctg ctg tat gtg cgg agg gag act gag gag gtg				1639
Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val	520	525	530	
ttt gac gcg ctc atg ttg aag acc cca gac ctg aag ggg ctg agg aat				1687
Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn	535	540	545	
gcg atc tct gag aag tat ggg ttc cct gaa gag aac att tac aaa gtc				1735
Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile Tyr Lys Val	550	555	560	
tac aag aaa tgc aag cga gga atc tta gtc aac atg gac aac aac atc				1783
Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile	565	570	575	
att cag cat tac agc aac cac gtc gcc ttc ctg ctg gac atg ggg gag				1831
Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu	580	585	590	595
ctg gac ggc aaa att cag atc atc ctt aag gag ctg taa				1870
Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu	600	605		

<210> 8  
 <211> 607  
 <212> PRT  
 <213> HUMAN

<220>  
 <221> misc\_feature  
 <222> (117)..(117)  
 <223> The 'Xaa' at location 117 stands for Leu, or Phe.

<220>  
 <221> misc\_feature  
 <222> (172)..(172)  
 <223> The 'Xaa' at location 172 stands for Thr.

<400> 8

DAVI251.001APC\_sequence listing.TXT

Met	Trp	Met	Asn	Ser	Ile	Leu	Pro	Ile	Phe	Leu	Phe	Arg	Ser	Val	Arg
1				5					10					15	
Leu	Leu	Lys	Asn	Asp	Pro	Val	Asn	Leu	Gln	Lys	Phe	Ser	Tyr	Thr	Ser
			20					25					30		
Glu	Asp	Glu	Ala	Trp	Lys	Thr	Tyr	Leu	Glu	Asn	Pro	Leu	Thr	Ala	Ala
		35					40					45			
Thr	Lys	Ala	Met	Met	Arg	Val	Asn	Gly	Asp	Asp	Asp	Ser	Val	Ala	Ala
	50					55					60				
Leu	Ser	Phe	Leu	Tyr	Asp	Tyr	Tyr	Met	Gly	Pro	Lys	Glu	Lys	Arg	Ile
65					70					75					80
Leu	Ser	Ser	Ser	Thr	Gly	Gly	Arg	Asn	Asp	Gln	Gly	Lys	Arg	Tyr	Tyr
				85					90					95	
His	Gly	Met	Glu	Tyr	Glu	Thr	Asp	Leu	Thr	Pro	Leu	Glu	Ser	Pro	Thr
			100					105					110		
His	Leu	Met	Lys	Xaa	Leu	Thr	Glu	Asn	Val	Ser	Gly	Thr	Pro	Glu	Tyr
		115					120					125			
Pro	Asp	Leu	Leu	Lys	Lys	Asn	Asn	Leu	Met	Ser	Leu	Glu	Gly	Ala	Leu
	130					135					140				
Pro	Thr	Pro	Gly	Lys	Ala	Ala	Pro	Leu	Pro	Ala	Gly	Pro	Ser	Lys	Leu
145					150					155					160
Glu	Ala	Gly	Ser	Val	Asp	Ser	Tyr	Leu	Leu	Pro	Xaa	Thr	Asp	Met	Tyr
				165					170					175	
Asp	Asn	Gly	Ser	Leu	Asn	Ser	Leu	Phe	Glu	Ser	Ile	His	Gly	Val	Pro
			180					185					190		
Pro	Thr	Gln	Arg	Trp	Gln	Pro	Asp	Ser	Thr	Phe	Lys	Asp	Asp	Pro	Gln
		195					200					205			
Glu	Ser	Met	Leu	Phe	Pro	Asp	Ile	Leu	Lys	Thr	Ser	Pro	Glu	Pro	Pro
	210					215					220				
Cys	Pro	Glu	Asp	Tyr	Pro	Ser	Leu	Lys	Ser	Asp	Phe	Glu	Tyr	Thr	Leu
225					230					235					240
Gly	Ser	Pro	Lys	Ala	Ile	His	Ile	Lys	Ser	Gly	Glu	Ser	Pro	Met	Ala
			245						250					255	

DAVI251.001APC\_sequence listing.TXT

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala  
 260 265 270  
 Gly Gly Lys Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val  
 275 280 285  
 Met Val Val Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe  
 290 295 300  
 Trp Lys His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile  
 305 310 315 320  
 Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Glu His Ile Glu  
 325 330 335  
 Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu  
 340 345 350  
 Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser  
 355 360 365  
 Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr  
 370 375 380  
 Asp Cys Gly Leu Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln  
 385 390 395 400  
 Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp  
 405 410 415  
 Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn  
 420 425 430  
 Ser Gly Val Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr  
 435 440 445  
 Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe  
 450 455 460  
 Ile Pro Asn Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala  
 465 470 475 480  
 Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr  
 485 490 495  
 Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala

DAVI251.001APC\_sequence listing.TXT

500

505

510

Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr  
515 520 525

Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly  
530 535 540

Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile  
545 550 555 560

Tyr Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp  
565 570 575

Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp  
580 585 590

Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu  
595 600 605

<210> 9  
<211> 3113  
<212> DNA  
<213> MURINE

<220>  
<221> misc\_feature  
<222> (2634)..(2634)  
<223> n = any nucleotide

<220>  
<221> misc\_feature  
<222> (2968)..(2968)  
<223> n = any nucleotide

<400> 9  
gttcctccat gggttccttg agttcctgac atggcttccc ttgatgatga actgtgtgac 60  
ctaaacagca taccaaattgt gacggagcag cccctcattt ctgctggaga aaacagggta 120  
caagtgtgta aaaacgtgcc cttcaacatc gtcctcccc atagcaacca gctgggcatt 180  
gataagagag gccatctgac agctcccgat acaacagtca ctgtctccat agcgaccatg 240  
cctaccact ccatcaagac agaaatccag ccgcacggct ttgctgtggg aatccctcca 300  
gccgtgtacc actctgagcc caccgaacgc gtggtggttt ttgaccggag cctcagcact 360  
gatcagttca gctctggcac tcagccccc aatgctcagc ggaggactcc agactccacc 420  
ttctccgaga cttcaagga gggcgttcag gaggttttct tcccctcgga actcagcctt 480  
cggatgccgg gcatgaattc agaggactat gtctttgaca atgtttctgg gaacaacttt 540

## DAVI251.001APC\_sequence listing.TXT

gagtataccc	tggaagcctc	caagtcactg	cggcagaagc	aaggggacag	cactatgaca	600
tacctgaata	aaggccagtt	ctatcctgtc	accttaaagg	aaggaagcag	caatgaaggg	660
attcaccacc	ctatcagcaa	agttcgaagt	gtgatcatgg	tggtttttgc	tgaagacaaa	720
agcagagaag	accagctgag	acactggaag	tactggcact	cccgtcagca	cacggccaaa	780
cagaggtgca	ttgacattgc	tgactacaaa	gaaagtttca	acactatcag	caacattgag	840
gagatagctt	ataacgccat	ttccttcacg	tgggacatca	atgatgaggc	aaagggtcttc	900
atctctgtga	actgcttgag	cacagatttc	tcttctcaga	aggggtgtgaa	gggcttgcca	960
ctcaacattc	aaatcgacac	atacagctat	aacaaccgca	gcaacaagcc	ggttcaccgg	1020
gcctactgcc	agataaagggt	cttctgcgac	aaggggagctg	aaaggaaaat	tcgggatgaa	1080
gaacgaaaac	agagcaagag	aaaagtgtct	gacgttaaag	tgacagctgct	tccttcacac	1140
aaacggacag	acatcacagt	gttcaagccc	ttcctggacc	tcgacactca	gcctgtcctc	1200
ttcattccgg	acgtgcattt	taccaacctg	cagcggggca	gtcatgttct	ttccctcccc	1260
tctgaagaac	tggaagggtga	aggctctgtc	ttgaaaagag	ggccattcgg	aaccgaagat	1320
gactttggag	ttcctcctcc	tgctaagctg	actcggacag	aagaacccaa	gagagtgtctg	1380
ctctatgtcc	gaaaggaatc	agaagaagtc	ttcgacgccc	tgatgctcaa	gacgccgtct	1440
ttgaagggcc	tgatggaggc	aatttcagac	aagtatgatg	tcccccata	caagattggg	1500
aaaatatatta	agaagtgcaa	aaaagggatc	ctcgtgaaca	tggaacgaaa	cattgtgaag	1560
cactactcca	atgaggacac	cttcagctg	cagatagagg	aagccggcgg	ctcgtacaag	1620
ctcacctga	cagagattta	aaggggcagg	gggtggggggc	gctcggctcc	caggcgtggg	1680
aattcagtga	aagtgttcca	gctgagaagc	ccaggcacct	accctgcaga	accttaaata	1740
tcaggggaagg	aacctttcac	gtaggaaatg	gcgctgtgta	taccgtgctg	tgttgatgtt	1800
ttcttttgga	tagaaatcca	tgtgttggtt	tggtgtgtgt	gtttgaattt	ctgatgtgct	1860
tagaaagcga	agcatgagaa	ctttgtaccg	gatctaagag	accatgggac	cgtttggggtt	1920
acctgctcca	ctacctgtca	aagtctgcct	gtgtccataa	gagtgggtggg	ctactggctg	1980
gcgagagagg	ggaaggcagt	agcttgtctt	tgaggctttt	gtgttctcgc	ctgacctcag	2040
tctaactctg	actgccttga	ggagtggggc	cagccctcag	caataaaggg	ctaagccttc	2100
tcctccacc	tctcctccag	tgtttactaa	atagggtgca	ttcctggaac	cttttcccgc	2160
aacttccctt	ggacatgtgg	actgcctttc	tgatgaagaa	cttgctgtgag	tgacagtgtg	2220
aagttagctc	tgtaaagct	gcgttggtata	taagtgaat	atctttttga	aggtctgcct	2280
gtaaatgtgt	acatatatgt	ctgatataaa	tatataatat	ataaatgcgg	tgtctgtgta	2340
cagatagtga	aggcgagcag	gaagatctac	cttgaaatcc	ctcttagaga	agaggttaag	2400
ttattattga	taatgtggac	caagcaggta	gaacgctgtt	ttcccaaaaa	caagcaagtg	2460



DAVI251.001APC\_sequence listing.TXT

```

ttccctagca tagcaaaaag ccattctcatg tggcagagcc atctgctctt gcgaatgttg 2520
tcaccgtgtg ggtttctgca ccctgagtgg agctaattgga agactggact gcagctacta 2580
tatgaggtgt gtgtgcaggt gtcagccaag ctgtgcccat gcagagactc agcngtgtca 2640
tgagccagcg attcaaacca aaatgggccg attctacaag gccatgtttc agagcttcca 2700
agcatcagct accgtgtgtt tgaactggaa ggcattcatg aatttacata actgtggcag 2760
gggaatgttt tgtgcacact taaatattta agaacaaaac gaaactttac aatgtaaytt 2820
tataatgaat cctgtaacag aaatacaatt gcgggtttct ttaggttcag ggaactagaa 2880
taggtcattt gtatgagtag gattgttagc ggtatacgta rgttaaaaag tactctaatt 2940
aagtatgtga acaaaatagc tggttttnta agatacggga tacgggtcat ataacaatat 3000
tttctatttt gttttatgaa atcagcttta cttgttttaa ttgtatcatt gaacatgtgt 3060
tttaaaccaa agggattgaa ttttatatgt ctatttcaaa aaaaaaaaaa aaa 3113

```

<210> 10  
 <211> 536  
 <212> PRT  
 <213> MURINE

<400> 10

Met Ala Ser Leu Asp Asp Glu Leu Cys Asp Leu Asn Ser Ile Pro Asn  
 1 5 10 15

Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val Gln Val  
 20 25 30

Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn Gln Leu  
 35 40 45

Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr Val Thr  
 50 55 60

Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu Ile Gln  
 65 70 75 80

Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His Ser Glu  
 85 90 95

Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr Asp Gln  
 100 105 110

Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr Pro Asp  
 115 120 125

## DAVI251.001APC\_sequence\_listing.TXT

Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val Phe Phe  
 130 135 140  
 Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu Asp Tyr  
 145 150 155 160  
 Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu Glu Ala  
 165 170 175  
 Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr Tyr Leu  
 180 185 190  
 Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser Ser Asn  
 195 200 205  
 Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val  
 210 215 220  
 Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys  
 225 230 235 240  
 Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile  
 245 250 255  
 Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile  
 260 265 270  
 Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys  
 275 280 285  
 Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys  
 290 295 300  
 Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr Ser Tyr  
 305 310 315 320  
 Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys  
 325 330 335  
 Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg  
 340 345 350  
 Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu Leu Pro  
 355 360 365  
 Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu Asp Leu  
 370 375 380

DAVI251.001APC\_sequence listing.TXT

Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr Asn Leu  
385 390 395 400

Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu Glu Gly  
405 410 415

Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp Asp Phe  
420 425 430

Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro Lys Arg  
435 440 445

Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu  
450 455 460

Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp  
465 470 475 480

Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys  
485 490 495

Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr  
500 505 510

Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly Gly Ser  
515 520 525

Tyr Lys Leu Thr Leu Thr Glu Ile  
530 535

<210> 11  
<211> 3452  
<212> DNA  
<213> MURINE

<220>  
<221> misc\_feature  
<222> (2973)..(2973)  
<223> n = any nucleotide

<220>  
<221> misc\_feature  
<222> (3307)..(3307)  
<223> n = any nucleotide

<400> 11  
cgccgctccg gaccaccgc ctgccgccgc gcgccgccgc ccgccgcctc ctccccccgg 60  
atcggtgtga ctgtcccaac ccgaaagtcc agttctgcgg ccgggcagcg gcgagcgagc 120

## DAVI251.001APC\_sequence listing.TXT

gcgatgacac	aggagtacga	caacaaaagg	cccgtgctgg	tacttcagaa	tgaagccctc	180
taccacacagc	ggcgctccta	taccagttag	gatgaagcct	ggaagtcggt	cctggaaaac	240
cctctcactg	cggcaaccaa	agcgatgatg	agcatcaacg	gagacgaaga	cagcgcggct	300
gcgctggggc	tgctctatga	ctactacaag	gtccccagag	agcgccggtc	atcagccgta	360
aagcccagagg	gagagcaccc	agagccagag	cacagcaaaa	gaaacagcat	accaaattgtg	420
acggagcagc	ccctcatttc	tgctggagaa	aacagggtag	aagtgtgtaa	aaacgtgccc	480
ttcaacatcg	tcctccccc	tagcaaccag	ctgggcattg	ataagagagg	ccatctgaca	540
gctcccgata	caacagtcac	tgtctccata	gcgaccatgc	ctacccactc	catcaagaca	600
gaaatccagc	cgcacggctt	tgctgtggga	atccctccag	ccgtgtacca	ctctgagccc	660
accgaacgcg	tggtgggttt	tgaccggagc	ctcagcactg	atcagttcag	ctctggcact	720
cagcccccca	atgctcagcg	gaggactcca	gactccacct	tctccgagac	cttcaaggag	780
ggcgttcagg	aggttttctt	cccctcggaa	ctcagccttc	ggatgccggg	catgaattca	840
gaggactatg	tctttgacaa	tgtttctggg	aacaactttg	agtataccct	ggaagcctcc	900
aagtcactgc	ggcagaagca	aggggacagc	actatgacat	acctgaataa	aggccagttc	960
tatcctgtca	ccttaaagga	aggaagcagc	aatgaaggga	ttcaccaccc	tatcagcaaa	1020
gttcgaagtg	tgatcatggt	ggtttttgct	gaagacaaaa	gcagagaaga	ccagctgaga	1080
cactggaagt	actggcactc	ccgtcagcac	acggccaaac	agaggtgcat	tgacattgct	1140
gactacaaag	aaagtttcaa	cactatcagc	aacattgagg	agatagctta	taacgccatt	1200
tccttcacgt	gggacatcaa	tgatgaggca	aaggctcttc	tctctgtgaa	ctgcttgagc	1260
acagatttct	cttctcagaa	gggtgtgaag	ggcttgccac	tcaacattca	aatcgacaca	1320
tacagctata	acaaccgcag	caacaagccg	gttcaccggg	cctactgcca	gataaagggtc	1380
ttctgcgaca	agggagctga	aaggaaaatt	cgggatgaag	aacgaaaaca	gagcaagaga	1440
aaagtgtctg	acgttaaagt	gcagctgctt	ccctcacaca	aacggacaga	catcacagtg	1500
ttcaagccct	tcctggacct	cgacactcag	cctgtcctct	tcattccgga	cggtgatttt	1560
accaacctgc	agcggggcag	tcattgttct	tccctcccct	ctgaagaact	ggaagggtgaa	1620
ggctctgtct	tgaaaagagg	gccattcgga	accgaagatg	actttggagt	tcctcctcct	1680
gctaagctga	ctcggacaga	agaaccaag	agagtgtctg	tctatgtccg	aaaggaatca	1740
gaagaagtct	tcgacgccct	gatgtctcaag	acgccgtctt	tgaagggcct	gatggaggca	1800
atttcagaca	agtatgatgt	ccccatgac	aagattggga	aaatatttaa	gaagtgcaaa	1860
aaagggatcc	tcgtgaacat	ggacgacaac	attgtgaagc	actactccaa	tgaggacacc	1920
ttccagctgc	agatagagga	agccggcggc	tcgtacaagc	tcaccctgac	agagatttaa	1980
aggggcaggg	gtggggggcg	ctcggctccc	aggcgtggga	attcagttaa	agtgttccag	2040

DAVI251.001APC\_sequence listing.TXT

```

ctgagaagcc caggcaccta ccctgcagaa ccttaaatat caggaagga acctttcacg 2100
taggaaatgg cgctgtgtat accgtgctgt gttgatgttt tcttttggat agaaatccat 2160
gtgtttgtttt gttgtttgttg tttgaatttc tgatgtgctt agaaagcgaa gcatgagaac 2220
tttgtaccgg atctaagaga ccatgggacc gtttggttta cctgctccac tacctgtcaa 2280
agtctgcctg tgtccataag agtggtgggc tactggctgg cgagagaggg gaaggcagta 2340
gcttgtcttt gaggtttttg tgttctcgcc tgacctcagt ctaactctga ctgccttgag 2400
gagtgggccc agccctcagc aataaagggc taagccttct ccctccacct ctccctcagt 2460
gtttactaaa tagggtgcat tcctggaacc ttttcccgca acttcccttg gacatgtgga 2520
ctgcctttct gatgaagaac ttgcgtgagt gacagtgtga agttagctct gttaaagctg 2580
cgttgtatat aagtgcata tctttttgaa ggtctgcctg taaatgtgta catatatgtc 2640
tgatataaat atataatata taaatgcggt gtctgtgtac agatagtga ggcgagcagg 2700
aagatctacc ttgaaatccc tcttagagaa gaggttaagt tattattgat aatgtggacc 2760
aagcaggtag aacgctgttt tcccaaaaac aagcaagtgt tccctagcat agcaaaaagc 2820
catctcatgt ggcagagcca tctgctcttg cgaatgttgt caccgtgtgg gtttctgcac 2880
cctgagtgga gctaattgaa gactggactg cagctactat atgaggtgtg tgtgcagggtg 2940
tcagccaagc tgtgcccatt cagagactca gcngtgtcat gagccagcga ttcaaaccaa 3000
aatgggccga ttctacaagg ccatgtttca gagcttccaa gcatcagcta ccgtgtgttt 3060
gaactggaag gcattcatga atttacataa ctgtggcagg ggaatgtttt gtgcacactt 3120
aaatatttaa gaacaaaacg aaactttaca atgtaayttt ataataatc ctgtaacaga 3180
aatacaattg cgggtttctt taggttcagg gaactagaat aggtcatttg tatgagtagg 3240
attgttagcg gtatacgtar gttaaaaagt actctaataga agtatgtgaa caaaatagct 3300
ggttttntaa gatacgggat acgggtcata taacaatatt ttctattttg ttttatgaaa 3360
tcagctttac ttgttttaaat tgtatcattg aacatgtgtt ttaaaccaaa gggattgaat 3420
tttatatgtc tatttcaaaa aaaaaaaaaa aa 3452

```

<210> 12  
 <211> 618  
 <212> PRT  
 <213> MURINE

<400> 12

Met Thr Gln Glu Tyr Asp Asn Lys Arg Pro Val Leu Val Leu Gln Asn  
 1 5 10 15

Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp Glu Ala  
 20 25 30

DAVI251.001APC\_sequence listing.TXT

Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met  
35 40 45

Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly Leu Leu  
50 55 60

Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Ala Val Lys  
65 70 75 80

Pro Glu Gly Glu His Pro Glu Pro Glu His Ser Lys Arg Asn Ser Ile  
85 90 95

Pro Asn Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val  
100 105 110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn  
115 120 125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr  
130 135 140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu  
145 150 155 160

Ile Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His  
165 170 175

Ser Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr  
180 185 190

Asp Gln Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr  
195 200 205

Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val  
210 215 220

Phe Phe Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu  
225 230 235 240

Asp Tyr Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu  
245 250 255

Glu Ala Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr  
260 265 270

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser

## DAVI251.001APC\_sequence listing.TXT

```

275                               280                               285
Ser Asn Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile
290                               295                               300

Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His
305                               310                               315                               320

Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile
325                               330                               335

Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu
340                               345                               350

Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu
355                               360                               365

Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
370                               375                               380

Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr
385                               390                               395                               400

Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
405                               410                               415

Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
420                               425                               430

Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu
435                               440                               445

Leu Pro Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu
450                               455                               460

Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr
465                               470                               475                               480

Asn Leu Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu
485                               490                               495

Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp
500                               505                               510

Asp Phe Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro
515                               520                               525

```

DAVI251.001APC\_sequence listing.TXT

Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp  
530 535 540

Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile  
545 550 555 560

Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys  
565 570 575

Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys  
580 585 590

His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly  
595 600 605

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile  
610 615

<210> 13  
<211> 2195  
<212> DNA  
<213> murine

<400> 13  
cgcccgggca ggtcagactt gaaagtccag tttcaccaga ggctgaggct ccaggaaaag 60  
gggagcgagt tcattggatc aaacatgtca caagagtcgg acaataataa aagactagtg 120  
gccttagtgc ccatgcccag tgaccctccc ttcaacaccc gaagagccta cacaagtgag 180  
gatgaggcct ggaagtcata tctggagaac cccctgactg cggccaccaa ggcatgatg 240  
agcatcaacg gggacgagga cagtgtgcc gccctgggcc tgctctatga ctactacaag 300  
gttcctcgag acaagagact tctgtctgtg agcaaagcaa gtgacagcca agaagaccag 360  
gataaaagaa actgccttgg caccagtga gcccagatca atttgagcgg aggcgagaac 420  
agagtgcagg ttctgaagac tgtcccgtg aacctctgtc taagtcaaga ccacatggag 480  
aattcgaagc gcgagcagta cagtgtatcc atcaccgaga gctctgccgt catccccgtg 540  
tcaggcatca ccgtggtgaa agccgaggat ttacaccgg tgttcatggc gcccccggtg 600  
cactatcccc gcgcggacag tgaggagcag cgcggtggtta tctttgaaca gactcagtac 660  
gacctgccct ccatagccag ccacagctcc tatctcaagg acgaccagcg cagcacgccg 720  
gacagcacct acagcgagag cttaaggagc ggcgcctcgg agaaatttcg gagtacttct 780  
gttggtgctg acgagtatac atatgaccag acgggaagtg gtacatttca gtacaccctg 840  
gaagccacca aatctctccg tcagaaacag ggggagggcc ccatgacctt cctcaacaaa 900  
ggacaattct atgccataac actcagttag actggagaca acaaattgctt ccgacacccc 960  
atcagcaaag tcaggagtgt ggtgatggtg gtctttagtg aagacaaaaa ccgagatgag 1020



DAVI251.001APC\_sequence listing.TXT

```

cagctgaaat actggaagta ctggcactcc cggcagcaca ctgccaagca gagggtcctt 1080
gacattgctg attacaagga gagcttcaac accatcggga acattgaaga gatcgcatat 1140
aatgctgttt ccttcacctg ggatgtgaac gagggaggcaa agatttttat caccgtgaat 1200
tgcctgagta cagatttctc ctcccaaaag ggtgtaaaag gacttcccct gatgattcag 1260
atcgacacgt acagctacaa caaccgcagc aataaaccca tccacagagc atactgccag 1320
atcaaggctt tctgtgacaa gggagcagaa agaaaaatcc gggatgaaga gagaaagcag 1380
aacaggaaga aagggaaggg ccaggcctct caagcccagt gcaacaactc ctctgatggg 1440
aagatggccg ccataccgtt acagaagaag agtgacatca cgtacttcaa aaccatgccc 1500
gacctgcact cacagcctgt gctcttcata ccagatgttc actttgcaaa cctacagagg 1560
accggacagg ttattataca cacagacgat gagcgagaag gcagcagcgt ccttgттааg 1620
cggatgttca ggcccatgga agaggagttt ggtccaacac cgtctaagca gatcaaagaa 1680
gaaaacgtaa aacgagtgtt ttatatgtg aggaaggaga acgatgacgt cttcgatgct 1740
ctgatgctga aatcacccac ggtgaagggg ctgatggaag cgctgtctga gaagtatggg 1800
ctgccagtgg agaaaatcac aaagctttat aagaagagca aaaagggcac cctggtcaac 1860
atggatgaca acatcattga gcactattca aatgaggaca ccttcacctt caacatggag 1920
agcatggtgg aaggcttcaa gatcacgctg atggagatct gagccctggg tgtcccctcg 1980
ataggagctt ttggtatact ccttcctggg agagatggga tctctgccgc cccaggacct 2040
ggagaccac ccattcact cacctctcaa gactgttaca agactgctgg gaaggggggc 2100
agggcccaag gccagtaat ggacttcctt caactcttcc acttgctccc tatggagctg 2160
aagcctgagc ccctcagcaa atttcttctc gtgcc 2195

```

<210> 14  
 <211> 625  
 <212> PRT  
 <213> murine

<400> 14

Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro  
 1 5 10 15

Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu  
 20 25 30

Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr  
 35 40 45

Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu  
 50 55 60

DAVI251.001APC\_sequence listing.TXT

Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu  
65 70 75 80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Asp Lys Arg Asn  
85 90 95

Cys Leu Gly Thr Ser Glu Ala Gln Ile Asn Leu Ser Gly Gly Glu Asn  
100 105 110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Cys Leu Ser Gln  
115 120 125

Asp His Met Glu Asn Ser Lys Arg Glu Gln Tyr Ser Val Ser Ile Thr  
130 135 140

Glu Ser Ser Ala Val Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala  
145 150 155 160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg  
165 170 175

Ala Asp Ser Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr  
180 185 190

Asp Leu Pro Ser Ile Ala Ser His Ser Ser Tyr Leu Lys Asp Asp Gln  
195 200 205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Gly Ala  
210 215 220

Ser Glu Lys Phe Arg Ser Thr Ser Val Gly Ala Asp Glu Tyr Thr Tyr  
225 230 235 240

Asp Gln Thr Gly Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys  
245 250 255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys  
260 265 270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys  
275 280 285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe  
290 295 300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp

DAVI251.001APC\_sequence\_listing.TXT

305		310		315		320
His	Ser	Arg	Gln	His	Thr	Ala
			325			
				Arg	Val	Leu
				330		
						Asp
						Ile
						Ala
						335
Tyr	Lys	Glu	Ser	Phe	Asn	Thr
			340			
						Ile
						Gly
						345
						Asn
						Ile
						Glu
						Glu
						Ala
						350
Asn	Ala	Val	Ser	Phe	Thr	Trp
		355				
						Asp
						360
						Val
						Asn
						Glu
						Glu
						Ala
						365
						Lys
						Ile
						Phe
Ile	Thr	Val	Asn	Cys	Leu	Ser
		370				
						Thr
						375
						Asp
						Phe
						Ser
						380
						Ser
						Gln
						Lys
						Gly
						Val
Lys	Gly	Leu	Pro	Leu	Met	Ile
					390	
						Gln
						Ile
						Asp
						395
						Thr
						Tyr
						Ser
						Tyr
						Asn
						400
Arg	Ser	Asn	Lys	Pro	Ile	His
				405		
						Arg
						Ala
						Tyr
						410
						Cys
						Gln
						Ile
						Lys
						Val
						415
						Phe
Cys	Asp	Lys	Gly	Ala	Glu	Arg
			420			
						Lys
						425
						Arg
						Asp
						Glu
						Glu
						Arg
						430
						Lys
						Gln
Asn	Arg	Lys	Lys	Gly	Lys	Gly
		435				
						Gln
						440
						Ala
						Ser
						Gln
						Ala
						445
						Cys
						Asn
						Asn
Ser	Ser	Asp	Gly	Lys	Met	Ala
		450				455
						Ala
						Ile
						Pro
						Leu
						Gln
						460
						Lys
						Lys
						Ser
						Asp
Ile	Thr	Tyr	Phe	Lys	Thr	Met
					470	
						Pro
						Asp
						Leu
						His
						475
						Ser
						Gln
						Pro
						Val
						Leu
						480
Phe	Ile	Pro	Asp	Val	His	Phe
				485		
						Ala
						Asn
						Leu
						490
						Gln
						Arg
						Thr
						Gly
						Gln
						495
						Val
Tyr	Tyr	Asn	Thr	Asp	Asp	Glu
			500			
						Arg
						Glu
						505
						Gly
						Ser
						Ser
						Val
						Leu
						510
						Val
						Lys
Arg	Met	Phe	Arg	Pro	Met	Glu
		515				
						Glu
						520
						Glu
						Phe
						Gly
						Pro
						525
						Thr
						Pro
						Ser
						Lys
Gln	Ile	Lys	Glu	Glu	Asn	Val
					530	
						Lys
						Arg
						Val
						Leu
						540
						Leu
						Tyr
						Val
						Arg
						Lys
Glu	Asn	Asp	Asp	Val	Phe	Asp
					550	
						Ala
						Leu
						Met
						Leu
						555
						Lys
						Ser
						Pro
						Thr
						Val
						560

DAVI251.001APC\_sequence\_listing.TXT

Lys Gly Leu Met Glu Ala Leu Ser Glu Lys Tyr Gly Leu Pro Val Glu  
565 570 575

Lys Ile Thr Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn  
580 585 590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile  
595 600 605

Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Ile Thr Leu Met Glu  
610 615 620

Ile  
625

<210> 15  
<211> 2831  
<212> DNA  
<213> murine

<220>  
<221> CDS  
<222> (200)..(2008)

<220>  
<221> misc\_feature  
<222> (2806)..(2806)  
<223> n = any nucleotide

<400> 15  
acctgtgctt ccagccaatc agcgccaccg cagccgggga ccgctgtcag caaaatctca 60  
acatccagag cgcaacgtag agcaaacgct tccccgggca ggaaggggaat gtctgtgtca 120  
gaggagaatt aagagacgag tggtcagcag cgcctgcgag ccaaccagag acggatcgct 180  
ggaacctcgg agaaggaag atg tcg aat gaa ctt gat ttc agg tct gtg cgg 232  
Met Ser Asn Glu Leu Asp Phe Arg Ser Val Arg  
1 5 10  
ttg ctg aag aat gac cct gtg agc ttc cag aag ttt ccc tac agt aat 280  
Leu Leu Lys Asn Asp Pro Val Ser Phe Gln Lys Phe Pro Tyr Ser Asn  
15 20 25  
gag gac gag gcc tgg aag aca tac ctg gag aac cct ttg acg gct gcc 328  
Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala  
30 35 40  
acc aaa gcc atg atg aga gtc aac ggg gac gag gag agt gtg gct gct 376  
Thr Lys Ala Met Met Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala  
45 50 55  
ctg agc ttc ctc tac gac tac tat atg ggt ccc aag gag aag cgg ata 424  
Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile  
60 65 70 75

## DAVI251.001APC\_sequence\_listing.TXT

ctg tcc tcc agc act ggt ggc cgg aat gac caa gga aag aag ttc tac	472
Leu Ser Ser Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr	
	80
cac agc atg gac tat gag ccg gat ctt gcc ccc ctc gag agc ccc aca	520
His Ser Met Asp Tyr Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr	
	95
cac ctc atg aaa ttt ttg aca gag aac gtg tct gga agt cca gac tac	568
His Leu Met Lys Phe Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr	
	110
aca gac cag ctc aag aaa aac aat ctg cta ggc ttg gag ggg gtt cta	616
Thr Asp Gln Leu Lys Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu	
	125
ccc acc ccc ggc aag acc aat acc gtc ccc cca ggt ccg agt aaa ctg	664
Pro Thr Pro Gly Lys Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu	
	140
gaa gcc agc tcc atg gac agc tac ctc ttg ccc gcc agt gac ata tat	712
Glu Ala Ser Ser Met Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr	
	160
gac aat ggc tcc ctc aac tca tta ttt gag agc att cat ggg gtt cca	760
Asp Asn Gly Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro	
	175
ccc aca cag cgc tgg cag cca gac agc acc ttc aaa gat gac cca cag	808
Pro Thr Gln Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln	
	190
gag tct ctg ctc ttc cct gat att ctg aag aca tcc ccg gac ccc cca	856
Glu Ser Leu Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Asp Pro Pro	
	205
tgc cca gag gat tat cca ggc ctc aag agt gac ttt gaa tac acc ctg	904
Cys Pro Glu Asp Tyr Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu	
	220
ggc tcc ccc aaa gcc att cac atc aaa gca ggg gag tca ccc atg gcc	952
Gly Ser Pro Lys Ala Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala	
	240
tac ctc aac aag ggt cag ttc tac ccc gtc acc cta cgc acc cca gca	1000
Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala	
	255
gga ggg aaa ggc ctc gct ctg tcc tcc agc aaa gtc aag agc gtg gtg	1048
Gly Gly Lys Gly Leu Ala Leu Ser Ser Lys Val Lys Ser Val Val	
	270
atg gtc gtg ttc gat aat gac aag gtc ccc gtg gag cag ctg cgt ttc	1096
Met Val Val Phe Asp Asn Asp Lys Val Pro Val Glu Gln Leu Arg Phe	
	285
tggtaggcac	1144
Trp Arg His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile	
	300
gac gta gct gac tgt aag gaa aac ttc aac acg gtc cag cac att gaa	1192
Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Gln His Ile Glu	
	320

## DAVI251.001APC\_sequence listing.TXT

gag gtg gcc tat aac gcg ctg tcc ttt gtg tgg aat gtc aac gag gaa	1240
Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu	
	335 340 345
gcc aag gtg ttt atc ggt gtc aac tgt ctg agc aca gac ttc tcc tcg	1288
Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser	
	350 355 360
cag aag gga gtg aag ggt gtc ccc ctg aac ttg caa att gac acc tat	1336
Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr	
	365 370 375
gac tgt gga gca ggc act gag cgc ctg gta cac cgt gct gtc tgc cag	1384
Asp Cys Gly Ala Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln	
	380 385 390 395
atc aag atc ttc tgt gat aag gga gct gag agg aag atg cgc gat gat	1432
Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp	
	400 405 410
gaa cgg aag cag ttt cga agg aag gtc aag tgc cca gac tcc agt aac	1480
Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn	
	415 420 425
aat gca gga atc aag ggc tgc ctg ctg tca ggc ttc agg ggc aat gag	1528
Asn Ala Gly Ile Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu	
	430 435 440
acc aca tac ttg cgg cca gaa act gac ctg gag acc cag cct gtg ttg	1576
Thr Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu	
	445 450 455
ttt atc ccc aat ctg cat ttt tcc agc cta cag cgc cca gga ggg gtt	1624
Phe Ile Pro Asn Leu His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val	
	460 465 470 475
gtc ccc tca gca gga cac agc agc tct gac agg ctg cct ctg aag cga	1672
Val Pro Ser Ala Gly His Ser Ser Ser Asp Arg Leu Pro Leu Lys Arg	
	480 485 490
acc tgc tca ccc ttt gct gag gag ttt gag cct ctt cct tct aaa caa	1720
Thr Cys Ser Pro Phe Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln	
	495 500 505
gcc aag gaa gat gac ctt cag aga gtt ctg ttg tat gtg agg agg gag	1768
Ala Lys Glu Asp Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu	
	510 515 520
aca gag gag gtg ttt gac gcg ctc atg ttg aag acc ccg gac ctg aag	1816
Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys	
	525 530 535
ggc ctg agg aat gcg atc tct gag aag tac ggc ctc ccc gag gag aat	1864
Gly Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn	
	540 545 550 555
att tgc aaa gtc tac aag aaa tgc aag cga ggc atc ctg gtt aac atg	1912
Ile Cys Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met	
	560 565 570
gac aac aac atc atc caa cac tac agc aac cac gtg gcc ttc ctg ctg	1960
Asp Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu	

## DAVI251.001APC\_sequence listing.TXT

575

580

585

gac atg ggt gag ctg gac ggc aag atc cag atc atc ctg aag gag cta 2008  
 Asp Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu  
 590 595 600  
 tgagggcccg gcctcaagcg tcccacaccc ggggcccggc tcaagccacg tacaacctct 2068  
 tctgtgtcag ctgttacttg aaatgccttt ctttgggaaa gaggtctcgc aagcaaccaa 2128  
 ctcggtgatg tccaagccag ggagagacca agaaggttcc aggatctaaa tgtccccacc 2188  
 aggctcgaac tcaactcaga gcttcctgaa agcaccacgc ccaccggaga gtctgagcaa 2248  
 cacagacca actgcctgct ttctcttcta agtcccgtcg cagaggccct tacaggggac 2308  
 gggggtcaca ccaccttctc tgcagggcta caccgctgt ctcgatcggg tctgacgttc 2368  
 actgtttcct ttctaccaac ttcagaccag agagtcttca cactttggcc aaataacttg 2428  
 aaaactcgtg actttcacag cagatgcctt tgtgaggccc ttggagagga aactttctta 2488  
 ttgacttcct cggcacaaga tgtaagtcac catcatcgag ctgacaggaa caataaccct 2548  
 tgccacctac tggtgtacac atttcttatt tacagttttc attatgtgat tatatatata 2608  
 tatatgtaag tatatattat gtacatatat gcaacatttt gtatgtccat gttacatttt 2668  
 tatcatttca aaaatatgta ttcatatttt cttgaactat ttttttagct gttattcgat 2728  
 tatgcatttt gtatatcata gggtttagta ataaaagcct acccatgcac acttaaaaaa 2788  
 aaaaaaaaaa aaatatchnag cttatcgata ccgtcgacct cga 2831

<210> 16  
 <211> 603  
 <212> PRT  
 <213> murine

<400> 16

Met Ser Asn Glu Leu Asp Phe Arg Ser Val Arg Leu Leu Lys Asn Asp  
1 5 10 15

Pro Val Ser Phe Gln Lys Phe Pro Tyr Ser Asn Glu Asp Glu Ala Trp  
20 25 30

Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met Met  
35 40 45

Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala Leu Ser Phe Leu Tyr  
50 55 60

Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser Ser Thr  
65 70 75 80

DAVI251.001APC\_sequence listing.TXT

Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr His Ser Met Asp Tyr  
85 90 95

Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr His Leu Met Lys Phe  
100 105 110

Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr Thr Asp Gln Leu Lys  
115 120 125

Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu Pro Thr Pro Gly Lys  
130 135 140

, Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu Glu Ala Ser Ser Met  
145 150 155 160

Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr Asp Asn Gly Ser Leu  
165 170 175

Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro Pro Thr Gln Arg Trp  
180 185 190

Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln Glu Ser Leu Leu Phe  
195 200 205

Pro Asp Ile Leu Lys Thr Ser Pro Asp Pro Pro Cys Pro Glu Asp Tyr  
210 215 220

Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser Pro Lys Ala  
225 230 235 240

Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala Tyr Leu Asn Lys Gly  
245 250 255

Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly Lys Gly Leu  
260 265 270

Ala Leu Ser Ser Ser Lys Val Lys Ser Val Val Met Val Val Phe Asp  
275 280 285

Asn Asp Lys Val Pro Val Glu Gln Leu Arg Phe Trp Arg His Trp His  
290 295 300

Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val Ala Asp Cys  
305 310 315 320

Lys Glu Asn Phe Asn Thr Val Gln His Ile Glu Glu Val Ala Tyr Asn  
325 330 335



DAVI251.001APC\_sequence listing.TXT

Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu Ala Lys Val Phe Ile  
340 345 350

Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val Lys  
355 360 365

Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys Gly Ala Gly  
370 375 380

Thr Glu Arg Leu Val His Arg Ala Val Cys Gln Ile Lys Ile Phe Cys  
385 390 395 400

Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp Glu Arg Lys Gln Phe  
405 410 415

Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn Asn Ala Gly Ile Lys  
420 425 430

Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu Arg  
435 440 445

Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu Phe Ile Pro Asn Leu  
450 455 460

His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val Val Pro Ser Ala Gly  
465 470 475 480

His Ser Ser Ser Asp Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro Phe  
485 490 495

Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Asp Asp  
500 505 510

Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val Phe  
515 520 525

Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn Ala  
530 535 540

Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn Ile Cys Lys Val Tyr  
545 550 555 560

Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile Ile  
565 570 575

Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu Leu  
580 585 590

DAVI251.001APC\_sequence listing.TXT

Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu  
595 600

<210> 17  
<211> 4840  
<212> DNA  
<213> drosophila

<400> 17  
aaaaatagaa aaaacaacaa caaattggct tgaaaacgca aatgccaggc gcaacgcccc 60  
cgaaccgacc cgccccctca acttttgcgc cctccagtag caatagcagc aatatgagca 120  
gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaag gcagcaccaa 180  
gcgaacgaaa caacaacagc tccacatacc acaagagtg gcacattaga agcggccaaa 240  
agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagcccc 300  
agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc 360  
accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca 420  
tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc 480  
acgatccagc tccagttcca ccgatccgat cactgtctcc agcgtgctcg agtgccatag 540  
atcctcacca agtgccaaaa tccgcatacct gatcccaaga gctcaaggca ccccggccca 600  
aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa 660  
acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag 720  
aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg ttataacttg 780  
ccagcagccg aggagcaac agcaatagca acaaccatag gggatcacgg catcgatgat 840  
cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg 900  
tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag 960  
ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc 1020  
cacagccgcc taggagttgg cgttggtggt ggcataccta gcgacgcac cctatcgccc 1080  
atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg 1140  
cccaacggag tgccacttct cacaacaatg caccgatcac cggactcac gcagccagaa 1200  
ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac 1260  
gacaaggagg ctgtatttat atacgaaacg cccaaggtgg tgatgccagc ggatggcggg 1320  
ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc 1380  
aaccaagccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaa 1440  
atcgagttcg atgagaacca gataatccgg gtggtgggac caaatggcga gcaacagcaa 1500  
atcatctcgc gggagatcat caatggggag catcatatcc tgtcgcgaaa cgaggctggt 1560

## DAVI251.001APC\_sequence listing.TXT

gagcacattc	tcacacggat	cgtcagtgat	ccctccaagt	tgatgcccac	tgacaatgca	1620
gtggccacgg	ccatgtacaa	ccaggcccaa	aagatgaaca	atgatcacgg	gcaggcggta	1680
tatcagacat	caccattgcc	gctagacgcg	tctgtattgc	attatagtgg	cggcaatgat	1740
tcgaatgtaa	ttaagacgga	ggccgatatc	tacgaggatc	acaagaaaca	tgcggtcgca	1800
gcagcagctg	ctgccggcgg	aggatccatc	atatacacca	catccgatcc	gaacggagtg	1860
aatgtgaaac	aactgcccc	tttgacggta	ccccaaaaac	ttgatcccga	cctctatcaa	1920
gccgataagc	atatagattt	gatctacaac	gatggcagca	agacggtgat	ttactccact	1980
acggatcaga	agagtttgga	aatatactcg	ggcggcgaca	tcggcagcct	ggtgtccgac	2040
ggccaagtgg	tggtccaggc	gggactgccg	tatgccacca	ccaccggagc	cggcggccag	2100
cccgtctata	tcgtggccga	cgggtgcctt	ccagcgggag	tcgaggagca	tctgcagagt	2160
ggaaagctca	atggccagac	cacacctatc	gatgtctctg	gcctatcgca	aaatgagatt	2220
caaggctttt	tgctcggctc	acacccctcg	tcatcggcga	cggtaagcac	aaccggcggt	2280
gtctccacga	caacgatctc	gcatcaccag	caacagcagc	agcagcagca	acagcaacag	2340
cagcagcagc	agcagcaaca	ccagcagcag	cagcaacatc	ccggcgacat	tgttagtgcc	2400
gctggcgctg	ggagcacggg	ctccattgtc	tcctctgcgg	cgcaacagca	gcagcagcag	2460
caactaatta	gcatcaaacg	agagcccga	gacttgcgca	aggatcccaa	gaatggcaac	2520
attgccggtg	cagcaacagc	aaatggaccc	ggttcggtca	taacccaaaa	gtcctttgat	2580
tatacggaat	tgtgccagcc	gggcacgctg	atcgatgcc	atggcagcat	acccgtcagc	2640
gtgaacagca	tccagcagag	aacggcggtc	catggcagcc	agaacagtcc	caccacatcg	2700
ctggtggaca	ccagcaccaa	tggatccacg	cgatcgcggc	cctggcacga	ctttggacgt	2760
cagaatgatg	ccgacaaaat	acaaatacca	aaaatcttca	caaacgtggg	cttccgatat	2820
cacctggaga	gccccatcag	ttcatcgcag	aggcgcgagg	acgatcgc	cacctacatc	2880
aacaagggtc	aattctatgg	aataacgctg	gagtatgtgc	acgatgcgga	aaagcccatt	2940
aagaacacca	ccgtcaagag	tgtgatcatg	ctaattgttc	gagaggagaa	gagtcccag	3000
gatgagatca	aggcctggca	attctggcac	agtcgtcagc	attccgtgaa	gcagagaatc	3060
ttggatgcag	atacgaagaa	ctcggttggc	ctcgttggct	gcatcgagga	agtgtcgcac	3120
aatgccatcg	ccgtctactg	gaatccgctg	gagagctccg	ccaagatcaa	cattgcgggt	3180
cagtgcctga	gcacggattt	cagcagtcaa	aagggaggcc	tgccgctgca	cgtacaaatc	3240
gacacatttg	aggaccccag	agatacggcg	gtcttccacc	gcggctactg	tcagataaag	3300
gtcttctgcg	ataagggcgc	cgaacgaaag	acgcgcgatg	aagagcggcg	ggccgccaaa	3360
cgaaagatga	cagccacggg	cagaaagaag	ctggacgagc	tttaccatcc	ggtaacggat	3420

## DAVI251.001APC\_sequence listing.TXT

```

cgggtccgagt tctatggcat gcaggacttc gccaaagccgc cgggtgctatt ctcgcccgcc 3480
gaggacatgg agaaggtagg tcagctgggc attggcgctg ccaccggcat gacattcaac 3540
cccctgagca acggcaactc caactccaac tcgcactcgt ccttgacagag cttctacggc 3600
catgagactg actcgccgga cctgaagggg gcctcaccgt tcctgctcca cggccagaag 3660
gtggccacgc cgacgtcaa gttccacaac cattttccgc ccgacatgca gaccgataag 3720
aaggatcaca tactggacca gaacatgttg accagcacac ccctgaccga ctttgggtccg 3780
ccgatgaagc gcggcaggat gacgccgccg acctcggaac gcgtgatgct gtacgtgcgg 3840
caggagaacg aggaggtgta tacaccgttg cacgtggtgc cggccaccac gatcggcctg 3900
ctaaatgcga ttgaaaacaa atacaaaatc tcaacaacga gcataaataa catttatcgc 3960
acaaacaaga aggggattac tgcgaaaatt gacgatgaca tgatatcggt ctactgcaac 4020
gaggacatct ttctgctgga ggtgcaacag atcgaggacg acctgtacga tgtgacgctc 4080
acggagctgc ccaatcagta gcgctggcag tacgggtagc acccgctaac cgcactcaaa 4140
aaaaaaagca aacaaacaca caaattacgg acacaacaag ttgtttcaat aagccatttt 4200
ccatagagcc taagtctaaa tatcgtagtt ataataatgg gatccgcaac aaatcgagtt 4260
gcaacgaatg ttaagaacgc taacacaata cgcagtataa atgatacttt aaaattgatt 4320
tagttatttt agcaacaatg agattatcta aaattgtttg atcaaatttt acattctcgc 4380
tatgtctata gataattcta agcccgtgag ccataagcg taatcgtaat cgtaatcgta 4440
ccgtgtattt atgctcatat ataaacaact atatatatat atatatatat atatatgtgc 4500
ggagtgcac agtgtctgtc cagtaggaga taagtctcgt ttccgctccc ctgcttatgc 4560
tatgacctta ggtccagggc aagtatgagt taccgaatct atctattagg tgcattcaac 4620
gaaaggaatc attagctctg cacgaactct agccgtagcc tattgtaatc catttgatg 4680
tttggtttaa gcgttttact tgttgaatat aaagtgtaaa attatttttg aaaaaaaaaa 4740
accacacaa aacacaaatc gtttgttcta tatttctgtt tcaaaactaa ctcgttacct 4800
acaatcccct ctgttatgta taattaggat ctctgtacac 4840

```

<210> 18  
 <211> 1061  
 <212> PRT  
 <213> murine

<400> 18

Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu  
 1 5 10 15

Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His  
 20 25 30

DAVI251.001APC\_sequence listing.TXT

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu  
35 40 45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser  
50 55 60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro  
65 70 75 80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu  
85 90 95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser  
100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val  
115 120 125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His  
130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln  
145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile  
165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu  
180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile  
195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser  
210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met  
225 230 235 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr  
245 250 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly  
260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp  
275 280 285

DAVI251.001APC\_sequence listing.TXT

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser  
290 295 300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu  
305 310 315 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala  
325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile  
340 345 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp  
355 360 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu  
370 375 380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val  
385 390 395 400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly  
405 410 415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln  
420 425 430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala  
435 440 445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His  
450 455 460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln  
465 470 475 480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala  
485 490 495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln  
500 505 510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg  
515 520 525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly

## DAVI251.001APC\_sequence\_listing.TXT

530  
 535  
 540  
 Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys  
 545 550 555 560  
 Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val  
 565 570 575  
 Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro  
 580 585 590  
 Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg  
 595 600 605  
 Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile  
 610 615 620  
 Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro  
 625 630 635 640  
 Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn  
 645 650 655  
 Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu  
 660 665 670  
 Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe  
 675 680 685  
 Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp  
 690 695 700  
 His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr  
 705 710 715 720  
 Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn  
 725 730 735  
 Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn  
 740 745 750  
 Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly  
 755 760 765  
 Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr  
 770 775 780

DAVI251.001APC\_sequence listing.TXT

Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys  
785 790 795 800

Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg  
805 810 815

Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro  
820 825 830

Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro  
835 840 845

Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Val Gly Gln Leu  
850 855 860

Gly Ile Gly Ala Ala Thr Gly Met Thr Phe Asn Pro Leu Ser Asn Gly  
865 870 875 880

Asn Ser Asn Ser Asn Ser His Ser Ser Leu Gln Ser Phe Tyr Gly His  
885 890 895

Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu His  
900 905 910

Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe Pro  
915 920 925

Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met  
930 935 940

Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly  
945 950 955 960

Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln  
965 970 975

Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr  
980 985 990

Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr  
995 1000 1005

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala  
1010 1015 1020

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile  
1025 1030 1035



DAVI251.001APC\_sequence listing.TXT

Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val  
1040 1045 1050

Thr Leu Thr Glu Leu Pro Asn Gln  
1055 1060

<210> 19  
<211> 21  
<212> DNA  
<213> human

<400> 19  
gaagtctttg atgccctgat g 21

<210> 20  
<211> 21  
<212> DNA  
<213> human

<220>  
<221> misc\_feature  
<223> human p49 mgr

<400> 20  
aaccattcc ctcgacatag a 21

<210> 21  
<211> 20  
<212> DNA  
<213> human

<400> 21  
agcgcgatga cacaggagta 20

<210> 22  
<211> 20  
<212> DNA  
<213> human

<400> 22  
cgttgctatg gagacagtga 20

<210> 23  
<211> 20  
<212> DNA  
<213> human

<400> 23  
ccgtttaaca aggacactgc 20

<210> 24  
<211> 20  
<212> DNA  
<213> murine

DAVI251.001APC\_sequence listing.TXT

<400> 24		
ctggaagcca ccaaattctt		20
<210> 25		
<211> 20		
<212> DNA		
<213> murine		
<400> 25		
agcgcgatga cacaggagta		20
<210> 26		
<211> 20		
<212> DNA		
<213> murine		
<400> 26		
agtgccagag ctgaactgat		20
<210> 27		
<211> 20		
<212> DNA		
<213> murine		
<400> 27		
tccatgggtt ccttgagttc		20
<210> 28		
<211> 20		
<212> DNA		
<213> murine		
<400> 28		
agtgccagag ctgaactgat		20
<210> 29		
<211> 20		
<212> DNA		
<213> murine		
<400> 29		
aaaggggagc gagttcattg		20
<210> 30		
<211> 20		
<212> DNA		
<213> murine		
<400> 30		
agagctctcg gtgatggata		20
<210> 31		
<211> 34		
<212> DNA		
<213> drosophila dopa decarboxylase promoter		

DAVI251.001APC\_sequence listing.TXT

<400> 31		
ggtggtgctc taataaccgg tttccaagat gcgc		34
<210> 32		
<211> 34		
<212> DNA		
<213> drosophila PCNA promoter		
<400> 32		
gggtaaaaag tgtgaacaat caaaccagtt ggca		34
<210> 33		
<211> 84		
<212> DNA		
<213> human		
<400> 33		
ggacacacac ccaaaccac acccaccac aaacacacaa accggcagtg acaacaacca		60
cccatccttc aataacagca acca		84
<210> 34		
<211> 4747		
<212> DNA		
<213> Drosophila		
<400> 34		
aaaaatagaa aaaacaacaa caaattggct tgaaaacgca aatgccaggc gcaacgcccc		60
cgaaccgacc cgccccctca acttttgcg cctccagtag caatagcagc aatatgagca		120
gcagcaacat caaatgttag gccaaaatgc acaaacggcc agcaacaaag gcagcaccaa		180
gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa		240
agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagcccc		300
agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc		360
accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca		420
tttcagttac agctccagac tcccagggtg cagactccca aagcaaacag actccagtcc		480
acgatccagc tccagttcca ccgatccgat cactgctcc agcgtgctcg agtgccatag		540
atcctcacca agtgccaaaa tccgcaccc gatcccaaga gctcaaggca ccccgccca		600
aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa		660
acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag		720
aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg ttataacttg		780
ccagcagccg aggagcaac agcaatagca acaaccatag gggatcacgg catcgatgat		840
cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg		900
tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag		960

## DAVI251.001APC\_sequence listing.TXT

ctctcgctgt	ccggccacgc	ccacggtcac	ggtcacgccc	accagttgca	ccagcacacc	1020
cacagccgcc	taggagttgg	cgttggtggt	ggcatcctta	gcgacgcatc	cctatcgccc	1080
atccaacaag	gcagtggcgg	ccacagcggc	ggaggtaaca	caaacagttc	accactggcg	1140
cccaacggag	tgccacttct	cacaacaatg	caccgatcac	cggactcacc	gcagccagaa	1200
ttggccacca	tgacgaacgt	caacgtgctg	gatctgcaca	cggataactc	caagctgtac	1260
gacaaggagg	ctgtatttat	atacgaaacg	ccaagggtgg	tgatgccagc	ggatggcggg	1320
ggtggcaata	attccgatga	aggtcatgcc	atcgatgcgc	ggattgcggc	ccaaatgggc	1380
aaccaagccc	agcaacagca	gcagcagcaa	cagcagacgg	aacaccagcc	gctggccaag	1440
atcgagttcg	atgagaacca	gataatccgg	gtggtgggac	caaatggcga	gcaacagcaa	1500
atcatctcgc	gggagatcat	caatggggag	catcatatcc	tgtcgcgaaa	cgaggctggt	1560
gagcacattc	tcacacggat	cgtcagtgat	ccctccaagt	tgatgccccaa	tgacaatgca	1620
gtggccacgg	ccatgtacaa	ccaggcccaa	aagatgaaca	atgatcacgg	gcaggcggta	1680
tatcagacat	caccattgcc	gctagacgcg	tctgtattgc	attatagtgg	cggcaatgat	1740
tcgaatgtaa	ttaagacgga	ggccgatatc	tacgaggatc	acaagaaaca	tgcggctgca	1800
gcagcagctg	ctgccggcgg	aggatccatc	atatacacca	catccgatcc	gaacggagtg	1860
aatgtgaaac	aactgccccca	tttgacggta	ccccaaaaac	ttgatcccga	cctctatcaa	1920
gccgataagc	atatagattt	gatctacaac	gatggcagca	agacggtgat	ttactccact	1980
acggatcaga	agagtttggga	aatatactcg	ggcggcgaca	tcggcagcct	ggtgtccgac	2040
ggccaagtgg	tggtccaggc	gggactgccg	tatgccacca	ccaccggagc	cggcggccag	2100
cccgtctata	tcgtggccga	cgggtgccttg	ccagcgggag	tcgaggagca	tctgcagagt	2160
ggaaagctca	atggccagac	cacacctatc	gatgtctctg	gcctatcgca	aaatgagatt	2220
caaggctttt	tgctcggctc	acacccctcg	tcatcggcga	cggtaagcac	aaccggcggt	2280
gtctccacga	caacgatctc	gcatcaccag	caacagcagc	agcagcagca	acagcaacag	2340
cagcagcagc	agcagcaaca	ccagcagcag	cagcaacatc	ccggcgacat	tgttagtgcc	2400
gctggcgtgg	ggagcacggg	ctccattgtc	tcctctgcgg	cgcaacagca	gcagcagcag	2460
caactaatta	gcatcaaacg	agagcccga	gacttgcgca	aggatcccaa	gaatggcaac	2520
attgccggtg	cagcaacagc	aaatggaccc	ggttcgggtca	taacccaaaa	gtcctttgat	2580
tatacggaat	tgtgccagcc	gggcacgctg	atcgatgcca	atggcagcat	acccgtcagc	2640
gtgaacagca	tccagcagag	aacggcggtc	catggcagcc	agaacagtcc	caccacatcg	2700
ctggtggaca	ccagcaccaa	tggatccacg	cgatcgcggc	cctggcacga	ctttggacgt	2760
cagaatgatg	ccgacaaaat	acaaatacca	aaaatcttca	caaacgtggg	cttccgatat	2820
cacctggaga	gccccatcag	ttcatcgcat	aggcgcgagg	acgatcgcat	cacctacatc	2880

## DAVI251.001APC\_sequence listing.TXT

aacaaggggc	aattctatgg	aataacgctg	gagtatgtgc	acgatgcgga	aaagcccatt	2940
aagaacacca	ccgtcaagag	tgtgatcatg	ctaattgttc	gcgaggagaa	gagtcccgag	3000
gatgagatca	aggcctggca	attctggcac	agtcgtcagc	attccgtgaa	gcagagaatc	3060
ttggatgcag	atacgaagaa	ctcggttggc	ctcgttggct	gcatcgagga	agtgtcgcac	3120
aatgccatcg	ccgtctactg	gaatccgctg	gagagctccg	ccaagatcaa	cattgcgggtt	3180
cagtgttga	gcacggattt	cagcagtcaa	aagggaggcc	tgccgctgca	cgtacaaatc	3240
gacacatttg	aggaccccag	agatacggcg	gtcttccacc	gcggctactg	tcagataaag	3300
gtcttctgcg	ataagggcgc	cgaacgaaag	acgcgcgatg	aagagcggcg	ggccgccaaa	3360
cgaagatga	cagccacggg	cagaaagaag	ctggacgagc	tttaccatcc	ggtaacggat	3420
cgggtccgagt	tctatggcat	gcaggacttc	gccaaagccgc	cgggtgctatt	ctcgcgccgc	3480
gaggacatgg	agaagagctt	ctacggccat	gagactgact	cgccggacct	gaagggggcc	3540
tcaccgttcc	tgctccacgg	ccagaagggtg	gccacgccga	cgctcaagtt	ccacaaccat	3600
tttccgccc	acatgcagac	cgataagaag	gatcacatac	tggaccagaa	catgttgacc	3660
agcacacccc	tgaccgactt	tgggtccgccg	atgaagcgcg	gcaggatgac	gccgccgacc	3720
tcggaacgcg	tgatgctgta	cgtgcggcag	gagaacgagg	aggtgtatac	accgttgcac	3780
gtggtgccgc	ccaccacgat	cggcctgcta	aatgcgattg	aaaacaaata	caaaatctca	3840
acaacgagca	taaataacat	ttatcgca	aacaagaagg	ggattactgc	gaaaattgac	3900
gatgacatga	tatcgttcta	ctgcaacgag	gacatctttc	tgctggaggt	gcaacagatc	3960
gaggacgacc	tgtacgatgt	gacgctcacg	gagctgccc	atcagtagcg	ctggcagtag	4020
gggtagcacc	cgctaaccgc	actcaaaaaa	aaaagcaaac	aaacacacaa	attacggaca	4080
caacaagttg	tttcaataag	ccattttcca	tagagcctaa	gtctaaatat	cgtagttata	4140
ataatgggat	ccgcaacaaa	tcgagttgca	acgaatgtta	agaacgctaa	cacaatacgc	4200
atgtaaaatg	atactttaaa	attgatttag	ttatttttagc	aacaatgaga	ttatctaaaa	4260
ttgtttgatc	aaattttaca	ttctcgctat	gtctatagat	aattctaagc	ccgtaagccc	4320
ataagcgtaa	tcgtaatcgt	aatcgtaccg	tgtatttatg	ctcatatata	aacaactata	4380
tatatatata	tatatatata	tatgtgcgga	gtgcaacagt	gtctgtccag	taggagataa	4440
gtctcgtttc	cgctcccctg	cttatgctat	gaccttaggt	ccagggcaag	tatgagttac	4500
cgaatctatc	tattaggtgc	atctaacgaa	aggaatcatt	agctctgcac	gaactctagc	4560
cgtagcctat	tgtaatccat	ttgtatgttt	ggcttaagcg	ttttacttgt	tgaatataaa	4620
gtgtaaaatt	atTTTTgaaa	aaaaaaaaacc	cacacaaaac	acaaatcggt	tgttctatat	4680
ttctgtttca	aaactaactc	gttaccacaca	atccccctctg	ttatgtataa	ttaggatctc	4740

tgtacac

<210> 35  
 <211> 1030  
 <212> PRT  
 <213> Drosophila

<400> 35

Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu  
 1 5 10 15

Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His  
 20 25 30

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu  
 35 40 45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser  
 50 55 60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro  
 65 70 75 80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu  
 85 90 95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser  
 100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val  
 115 120 125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His  
 130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln  
 145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile  
 165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu  
 180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile  
 195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser

## DAVI251.001APC\_sequence\_listing.TXT

210  
 215  
 220  
 Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met  
 225 230 235 240  
 Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr  
 245 250 255  
 Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly  
 260 265 270  
 Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp  
 275 280 285  
 His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser  
 290 295 300  
 Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu  
 305 310 315 320  
 Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala  
 325 330 335  
 Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile  
 340 345 350  
 Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp  
 355 360 365  
 Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu  
 370 375 380  
 Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val  
 385 390 395 400  
 Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly  
 405 410 415  
 Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln  
 420 425 430  
 Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala  
 435 440 445  
 Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His  
 450 455 460

## DAVI251.001APC\_sequence\_listing.TXT

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln  
 465 470 475 480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala  
 485 490 495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln  
 500 505 510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg  
 515 520 525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly  
 530 535 540

Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys  
 545 550 555 560

Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val  
 565 570 575

Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro  
 580 585 590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg  
 595 600 605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile  
 610 615 620

Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro  
 625 630 635 640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn  
 645 650 655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu  
 660 665 670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe  
 675 680 685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp  
 690 695 700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr  
 705 710 715 720



DAVI251.001APC\_sequence listing.TXT

Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn  
                     725                    730                    735  
 Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn  
                     740                    745                    750  
 Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly  
                     755                    760                    765  
 Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr  
                     770                    775                    780  
 Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys  
                     785                    790                    795                    800  
 Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg  
                     805                    810  
 Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro  
                     820                    825                    830  
 Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro  
                     835                    840                    845  
 Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Ser Phe Tyr Gly  
                     850                    855                    860  
 His Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu  
                     865                    870                    875                    880  
 His Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe  
                     885                    890                    895  
 Pro Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn  
                     900                    905                    910  
 Met Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg  
                     915                    920                    925  
 Gly Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg  
                     930                    935                    940  
 Gln Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr  
                     945                    950                    955                    960  
 Thr Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr  
                     965                    970                    975

DAVI251.001APC\_sequence listing.TXT

Thr Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala  
 980 985 990

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile Phe  
 995 1000 1005

Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val Thr  
 1010 1015 1020

Leu Thr Glu Leu Pro Asn Gln  
 1025 1030

<210> 36  
 <211> 5650  
 <212> DNA  
 <213> Drosophila

<400> 36  
 aaaaatagaa aaaacaacaa caaattggct tgaaaacgca aatgccaggc gcaacgcccc 60  
 cgaaccgacc cgccccctca acttttgccg cctccagtag caatagcagc aatatgagca 120  
 gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaaag gcagcaccaa 180  
 gcgaacgaaa caacaacagc tccacatacc acaagagtg gcacattaga agcggccaaa 240  
 agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagcccc 300  
 agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc 360  
 accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca 420  
 tttcagttac agctccagac tcccagggtg cagactccca aagcaaacag actccagtcc 480  
 acgatccagc tccagttcca ccgatccgat cactgtctcc agcgtgctcg agtgccatag 540  
 atcctcacca agtgccaaaa tccgcatcct gatcccaaga gctcaaggca ccccggccca 600  
 aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa 660  
 acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag 720  
 aaaccacaaa gtgccttcca tcaatccggt gataagtgat atttattatg ttataacttg 780  
 ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat 840  
 cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg 900  
 tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag 960  
 ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc 1020  
 cacagccgcc taggagttgg cgttggtggt ggcacacctta gcgacgcac cctatcgccc 1080  
 atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg 1140  
 cccaacggag tgccacttct cacaacaatg caccgatcac cggactcacc gcagccagaa 1200

## DAVI251.001APC\_sequence listing.TXT

ttggccacca	tgacgaacgt	caacgtgctg	gatctgcaca	cggataactc	caagctgtac	1260
gacaaggagg	ctgtatttat	atacgaacg	cccaagggtg	tgatgccagc	ggatggcggg	1320
ggtggcaata	attccgatga	aggatcatgcc	atcgatgcgc	ggattgcggc	ccaaatgggc	1380
aaccaagccc	agcaacagca	gcagcagcaa	cagcagacgg	aacaccagcc	gctggccaag	1440
atcgagttcg	atgagaacca	gataatccgg	gtggtgggac	caaatggcga	gcaacagcaa	1500
atcatctcgc	gggagatcat	caatggggag	catcatatcc	tgtcgcgaaa	cgaggctggt	1560
gagcacattc	tcacacggat	cgtcagtgat	ccctccaagt	tgatgcccc	tgacaatgca	1620
gtggccacgg	ccatgtacaa	ccaggcccaa	aagatgaaca	atgatcacgg	gcaggcggta	1680
tatcagacat	caccattgcc	gctagacgcg	tctgtattgc	attatagtgg	cggcaatgat	1740
tcgaatgtaa	ttaagacgga	ggccgatatc	tacgaggatc	acaagaaaca	tgcggtcgca	1800
gcagcagctg	ctgccggcgg	aggatccatc	atatacacca	catccgatcc	gaacggagtg	1860
aatgtgaaac	aactgcccc	tttgacggta	ccccaaaaac	ttgatcccga	cctctatcaa	1920
gccgataagc	atatagattt	gatctacaac	gatggcagca	agacgggtgat	ttactccact	1980
acggatcaga	agagtttgga	aataactcgc	ggcggcgaca	tcggcagcct	ggtgtccgac	2040
ggccaagtgg	tggtccaggc	gggactgccg	tatgccacca	ccaccggagc	cggcggccag	2100
cccgtctata	tcgtggccga	cgggtgccttg	ccagcgggag	tcgaggagca	tctgcagagt	2160
ggaaagctca	atggccagac	cacacctatc	gatgtctctg	gcctatcgca	aaatgagatt	2220
caaggctttt	tgctcggttc	acacccctcg	tcatcggcga	cggtaagcac	aaccggcggt	2280
gtctccacga	caacgatctc	gcatcaccag	caacagcagc	agcagcagca	acagcaacag	2340
cagcagcagc	agcagcaaca	ccagcagcag	cagcaacatc	ccggcgacat	tgtagtgcc	2400
gctggcgtgg	ggagcacggg	ctccattgtc	tcctctgcgg	cgcaacagca	gcagcagcag	2460
caactaatta	gcatcaaacg	agagcccgaa	gacttgcgca	aggatcccaa	gaatggcaac	2520
attgccggtg	cagcaacagc	aaatggaccc	ggttcggtca	taacccaaaa	gatcttgcac	2580
gtggatgcac	caacggcaag	tgaagctgat	aggcccagca	caccagcag	cagcatcaac	2640
agcactgaaa	acactgaatc	ggactcacag	tcagtatcag	gatcagaatc	aggatcgccg	2700
ggagccagga	ccacagccac	actagagatg	tatgcaacca	cgggcggcac	acagatctat	2760
ctacagacct	cacatcccag	cacggcgagc	ggagcgggag	gcggcgccgg	acccgctgga	2820
gccgccggcg	gcggcggtgt	gtccatgcag	gcgcaaagtc	ccagtccggg	tcctatatatc	2880
acggccaatg	actatggcat	gtacacggcc	agtcgcctgc	caccgggtcc	cccggccacc	2940
agcaccacca	cgtttatagc	ggagccctcc	tactatcggg	aatactttgc	accggatggc	3000
caagggtggct	atgtgccggc	cagcacgagg	tctttgtatg	gcgacgtgga	cgtatccgta	3060

## DAVI251.001APC\_sequence listing.TXT

tctcagcccg	gcgagtggt	cacctatgag	ggccgctttg	ccggcagcgt	tccccgccc	3120
gccaccacca	ccgtgctaac	cagcgtgcat	caccaccagc	aacagcagca	gcaacaacag	3180
cagcatcaac	agcagcagca	gcagcaacag	caccaccagc	agcaacagca	ccattcgcag	3240
gatggcaaga	gcaatggcgg	agcaacgcca	ctctatgcca	aagccattac	ggcggcgggt	3300
ctaacggtgg	atttgccaag	tccggattcg	ggcattggta	cggatgccat	tacaccgcgg	3360
gatcagacaa	atatccaaca	gtcctttgat	tatacggaa	tgtgccagcc	gggcacgctg	3420
atcgatgcca	atggcagcat	acccgtcagc	gtgaacagca	tccagcagag	aacggcggtc	3480
catggcagcc	agaacagtcc	caccacatcg	ctggtggaca	ccagcaccaa	tggatccacg	3540
cgatcgcggc	cctggcacga	ctttggacgt	cagaatgatg	ccgacaaaat	acaataacca	3600
aaaatcttca	caaacgtggg	cttccgatat	cacctggaga	gccccatcag	ttcatcgcag	3660
aggcgcgagg	acgatcgcat	cacctacatc	aacaagggtc	aattctatgg	aataacgctg	3720
gagtatgtgc	acgatgcgga	aaagcccatt	aagaacacca	ccgtcaagag	tgtgatcatg	3780
ctaattgttcc	gcgaggagaa	gagtcccag	gatgagatca	aggcctggca	attctggcac	3840
agtcgtcagc	attccgtgaa	gcagagaatc	ttggatgcag	atacgaagaa	ctcggttggc	3900
ctcgttggct	gcatcgagga	agtgtcgcac	aatgccatcg	ccgtctactg	gaatccgctg	3960
gagagctccg	ccaagatcaa	cattgcggtt	cagtgccttga	gcacggattt	cagcagtcaa	4020
aaggaggagg	tgccgctgca	cgtacaaatc	gacacatttg	aggaccccag	agatacggcg	4080
gtctttccacc	gcggctactg	tcagataaag	gtcttctgcg	ataagggcgc	cgaacgaaag	4140
acgcgcgatg	aagagcggcg	ggccgccaaa	cgaaagatga	cagccacggg	cagaaagaag	4200
ctggacgagc	tttaccatcc	ggtaacggat	cggcccgagt	tctatggcat	gcaggacttc	4260
gccaagccgc	cggtgctatt	ctcgcccgcc	gaggacatgg	agaaggtagg	tcagctgggc	4320
attggcgctg	ccaccggcat	gacattcaac	cccctgagca	acggcaactc	caactccaac	4380
tcgcactcgt	ccttgacagag	cttctacggc	catgagactg	actcgccgga	cctgaagggg	4440
gcctcaccgt	tcttgctcca	cggccagaag	gtggccacgc	cgacgctcaa	gttcacaaac	4500
cattttccgc	ccgacatgca	gaccgataag	aaggatcaca	tactggacca	gaacatgttg	4560
accagcacac	ccctgaccga	ctttggtccg	ccgatgaagc	gcggcaggat	gacgccgccg	4620
acctcggaac	gcgtgatgct	gtacgtgcgg	caggagaacg	aggagggtga	tacaccgttg	4680
cacgtggtgc	cgccccaccac	gatcggcctg	ctaaatgcga	ttgaaaacaa	atacaaaatc	4740
tcaacaacga	gcataaataa	catttatcgc	acaaacaaga	aggggattac	tgcgaaaatt	4800
gacgatgaca	tgatatcggt	ctactgcaac	gaggacatct	ttctgctgga	ggtgcaacag	4860
atcgaggacg	acctgtacga	tgtgacgctc	acggagctgc	ccaatcagta	gcgctggcag	4920
tacgggtagc	acccgctaac	cgcactcaaa	aaaaaaagca	aacaaacaca	caaattacgg	4980

DAVI251.001APC\_sequence listing.TXT

```

acacaacaag ttgtttcaat aagccatttt ccatagagcc taagtctaaa tatcgtagtt 5040
ataataatgg gatccgcaac aaatcgagtt gcaacgaatg ttaagaacgc taacacaata 5100
cgcattgtaaa atgatacttt aaaattgatt tagttatttt agcaacaatg agattatcta 5160
aaattgtttg atcaaatttt acattctcgc tatgtctata gataattcta agcccgtaag 5220
cccataagcg taatcgtaat cgtaatcgta ccggtgtattt atgctcatat ataaacaact 5280
atatatatat atatatatat atatattgtg ggagtgcaac agtgtctgtc cagtaggaga 5340
taagtctcgt ttccgctccc ctgcttatgc tatgacctta ggtccagggc aagtatgagt 5400
taccgaatct atctattagg tgcattctaac gaaaggaatc attagctctg cacgaactct 5460
agccgtagcc tattgtaatc catttgtagt tttggcttaa gcgttttact tgttgaatat 5520
aaagtgtaaa attatttttg aaaaaaaaaa acccacacaa aacacaaatc gtttgttcta 5580
tatttctgtt tcaaaactaa ctcgttacct acaatcccct ctgttatgta taattaggat 5640
ctctgtacac 5650

```

```

<210> 37
<211> 1331
<212> PRT
<213> Drosophila
<400> 37

```

```

Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
1          5          10          15

```

```

Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
          20          25          30

```

```

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
          35          40          45

```

```

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
          50          55          60

```

```

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65          70          75          80

```

```

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
          85          90          95

```

```

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
          100          105          110

```

```

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
          115          120          125

```

DAVI251.001APC\_sequence listing.TXT

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His  
130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln  
145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile  
165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu  
180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile  
195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser  
210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met  
225 230 235 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr  
245 250 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly  
260 265 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp  
275 280 285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser  
290 295 300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu  
305 310 315 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala  
325 330 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile  
340 345 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp  
355 360 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu

DAVI251.001APC\_sequence\_listing.TXT

```

370                                     375                                     380
Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385                                     390                                     395                                     400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
405                                     410                                     415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
420                                     425                                     430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
435                                     440                                     445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
450                                     455                                     460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465                                     470                                     475                                     480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
485                                     490                                     495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
500                                     505                                     510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
515                                     520                                     525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
530                                     535                                     540

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
545                                     550                                     555                                     560

Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser
565                                     570                                     575

Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser
580                                     585                                     590

Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr
595                                     600                                     605

Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala
610                                     615                                     620

```

DAVI251.001APC\_sequence\_listing.TXT

Ser Gly Ala Gly Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly Gly  
625 630 635 640

Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr  
645 650 655

Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro  
660 665 670

Pro Pro Thr Ser Thr Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg  
675 680 685

Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr  
690 695 700

Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly  
705 710 715 720

Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala  
725 730 735

Thr Thr Thr Val Leu Thr Ser Val His His His Gln Gln Gln Gln Gln  
740 745 750

Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Gln His His Gln  
755 760 765

Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr  
770 775 780

Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu  
785 790 795 800

Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp  
805 810 815

Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro  
820 825 830

Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser  
835 840 845

Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr  
850 855 860

Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp  
865 870 875 880



DAVI251.001APC\_sequence listing.TXT

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys  
885 890 895

Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro Ile Ser  
900 905 910

Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly  
915 920 925

Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro  
930 935 940

Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu  
945 950 955 960

Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser  
965 970 975

Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn  
980 985 990

Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn Ala Ile  
995 1000 1005

Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn Ile  
1010 1015 1020

Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly  
1025 1030 1035

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp  
1040 1045 1050

Thr Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys  
1055 1060 1065

Asp Lys Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala  
1070 1075 1080

Ala Lys Arg Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu  
1085 1090 1095

Leu Tyr His Pro Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln  
1100 1105 1110

Asp Phe Ala Lys Pro Pro Val Leu Phe Ser Pro Ala Glu Asp Met  
1115 1120 1125

DAVI251.001APC\_sequence listing.TXT

Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr  
1130 1135 1140

Phe Asn Pro Leu Ser Asn Gly Asn Ser Asn Ser Asn Ser His Ser  
1145 1150 1155

Ser Leu Gln Ser Phe Tyr Gly His Glu Thr Asp Ser Pro Asp Leu  
1160 1165 1170

Lys Gly Ala Ser Pro Phe Leu Leu His Gly Gln Lys Val Ala Thr  
1175 1180 1185

Pro Thr Leu Lys Phe His Asn His Phe Pro Pro Asp Met Gln Thr  
1190 1195 1200

Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr  
1205 1210 1215

Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly Arg Met Thr  
1220 1225 1230

Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln Glu Asn  
1235 1240 1245

Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr Ile  
1250 1255 1260

Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr  
1265 1270 1275

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala  
1280 1285 1290

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile  
1295 1300 1305

Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val  
1310 1315 1320

Thr Leu Thr Glu Leu Pro Asn Gln  
1325 1330

<210> 38  
<211> 5557  
<212> DNA  
<213> Drosophila

## DAVI251.001APC\_sequence listing.TXT

```

<400> 38
aaaaatagaa aaaacaacaa caaattggct tgaaaacgca aatgccaggc gcaacgcccc 60
cgaaccgacc cgccccctca acttttgcgc cctccagtag caatagcagc aatatgagca 120
gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaag gcagcaccaa 180
gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa 240
agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagcccc 300
agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc 360
accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca 420
tttcagttac agctccagac tcccagggtg cagactccca aagcaaacag actccagtcc 480
acgatccagc tccagttcca ccgatccgat cactgtctcc agcgtgctcg agtgccatag 540
atcctcacca agtgccaaaa tccgcatact gatcccaaga gctcaaggca ccccggccca 600
aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa 660
acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag 720
aaaccacaaa gtgccttcca tcaatccggt gataagtgat atttattatg ttatacttg 780
ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat 840
cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg 900
tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag 960
ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc 1020
cacagccgcc taggagttgg cgttggtggt ggcataccta gcgacgcata cctatcgccc 1080
atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg 1140
cccaacggag tgccacttct cacaacaatg caccgatcac cggactcac gcagccagaa 1200
ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac 1260
gacaaggagg ctgtatttat atacgaaacg cccaagggtg tgatgccagc ggatggcggg 1320
ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc 1380
aaccaagccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaag 1440
atcgagttcg atgagaacca gataatccgg gtggtgggac caaatggcga gcaacagcaa 1500
atcatctcgc gggagatcat caatggggag catcatatcc tgtcgcgaaa cgaggctggt 1560
gagcacattc tcacacggat cgtcagtgat ccctccaagt tgatgcccaa tgacaatgca 1620
gtggccacgg ccatgtacaa ccaggcccaa aagatgaaca atgatcacgg gcaggcggta 1680
tatcagacat caccattgcc gctagacgcg tctgtattgc attatagtgg cggcaatgat 1740
tcgaatgtaa ttaagacgga ggccgatatc tacgaggatc acaagaaaca tgcggctgca 1800
gcagcagctg ctgccggcgg aggatccatc atatacacca catccgatcc gaacggagtg 1860

```

## DAVI251.001APC\_sequence listing.TXT

aatgtgaaac aactgcccc tttgacggtg ccccaaaaac ttgatcccga cctctatcaa	1920
gccgataagc atatagattt gatctacaac gatggcagca agacggtgat ttactccact	1980
acggatcaga agagtttgga aatatactcg ggcggcgaca tcggcagcct ggtgtccgac	2040
ggccaagtgg tgggtccaggc gggactgccc tatgccacca ccaccggagc cggcggccag	2100
cccgtctata tcgtggccga cgggtgccttg ccagcgggag tcgaggagca tctgcagagt	2160
ggaaagctca atggccagac cacacctatc gatgtctctg gcctatcgca aaatgagatt	2220
caaggctttt tgctcggctc acaccctcg tcatcggcga cggtaagcac aaccggcggt	2280
gtctccacga caacgatctc gcatcaccag caacagcagc agcagcagca acagcaacag	2340
cagcagcagc agcagcaaca ccagcagcag cagcaacatc ccggcgacat tgtagtgcc	2400
gctggcggtg ggagcacggg ctccattgtc tcctctgcgg cgcaacagca gcagcagcag	2460
caactaatta gcatcaaacg agagcccgaa gacttgcgca aggatcccaa gaatggcaac	2520
attgccggtg cagcaacagc aaatggaccc ggttcggtca taaccacaaa gatcttgac	2580
gtggatgcac caacggcaag tgaagctgat aggccagca caccagcag cagcatcaac	2640
agcactgaaa aactgaatc ggactcacag tcagtatcag gatcagaatc aggatcgccg	2700
ggagccagga ccacagccac actagagatg tatgcaacca cgggcggcac acagatctat	2760
ctacagacct cacatccag cacggcgagc ggagcgggcg gcggcgccgg acccgctgga	2820
gccgccggcg gcggcggtgt gtccatgcag gcgcaaagtc ccagtccggg tccctatc	2880
acggccaatg actatggcat gtacacggcc agtcgcctgc caccgggtcc cccgccacc	2940
agcaccacca cgtttatagc ggagccctcc tactatcggg aatactttgc accggatggc	3000
caagggtggt atgtgccggc cagcacgagg tctttgtatg gcgacgtgga cgtatccgta	3060
tctcagcccg gcggagtggg cacctatgag ggccgctttg ccggcagcgt tccccgccc	3120
gccaccacca ccgtgctaac cagcgtgcat caccaccagc aacagcagca gcaacaacag	3180
cagcatcaac agcagcagca gcagcaacag caccaccagc agcaacagca ccattcgag	3240
gatggcaaga gcaatggcgg agcaacgcca ctctatgcca aagccattac ggcggcgggt	3300
ctaacggtgg atttgccaa tccggattcg ggcattggta cggatgccat tacaccgagg	3360
gatcagacaa atatccaaca gtcctttgat tatacggaat tgtgccagcc gggcacgctg	3420
atcgatgcca atggcagcat accgctcagc gtgaacagca tccagcagag aacggcggtc	3480
catggcagcc agaacagtcc caccacatcg ctggtggaca ccagcaccaa tggatccacg	3540
cgatcgcggc cctggcacga ctttgacgt cagaatgatg ccgacaaaat acaaatacca	3600
aaaatcttca caaacgtggg cttccgatat cacctggaga gccccatcag ttcacgcag	3660
aggcgcgagg acgatcgcat cacctacatc aacaagggtc aattctatgg aataacgctg	3720
gagtatgtgc acgatgcgga aaagcccatt aagaacacca ccgtcaagag tgtgatcatg	3780

## DAVI251.001APC\_sequence listing.TXT

ctaattgttcc	gcgaggagaa	gagtgccgag	gatgagatca	aggcctggca	attctggcac	3840
agtcgtcagc	attccgtgaa	gcagagaatc	ttggatgcag	atacgaagaa	ctcggttggc	3900
ctcgttggct	gcattcgagga	agtgtcgcac	aatgccatcg	ccgtctactg	gaatccgctg	3960
gagagctccg	ccaagatcaa	cattgcgggtt	cagtgccttg	gcacggattt	cagcagtcaa	4020
aagggaggcc	tgccgctgca	cgtacaaatc	gacacatttg	aggaccccag	agatacggcg	4080
gtctttccacc	gcggctactg	tcagataaag	gtctttctgcg	ataagggcgc	cgaacgaaag	4140
acgcgcgatg	aagagcggcg	ggccgccaaa	cgaaagatga	cagccacggg	cagaaagaag	4200
ctggacgagc	tttaccatcc	ggtaacggat	cgggccgagt	tctatggcat	gcaggacttc	4260
gccaagccgc	cgggtgctatt	ctcgcccgcc	gaggacatgg	agaagagctt	ctacggccat	4320
gagactgact	cgccggacct	gaagggggcc	tcaccgttcc	tgctccacgg	ccagaagggtg	4380
gccacgccga	cgctcaagtt	ccacaaccat	tttccgccc	acatgcagac	cgataagaag	4440
gatcacatac	tggaaccagaa	catgttgacc	agcacacccc	tgaccgactt	tggtccgccg	4500
atgaagcgcg	gcaggatgac	gccgcccacc	tcggaacgcg	tgatgctgta	cgtgcggcag	4560
gagaacgagg	aggtgtatac	accgttgcac	gtggtgccgc	ccaccacgat	cggcctgcta	4620
aatgcgattg	aaaacaaata	caaaatctca	acaacgagca	taaataacat	ttatcgcaca	4680
aacaagaagg	ggattactgc	gaaaattgac	gatgacatga	tatcgtttcta	ctgcaacgag	4740
gacatctttc	tgctggagggt	gcaacagatc	gaggacgacc	tgtacgatgt	gacgctcacg	4800
gagctgcca	atcagtagcg	ctggcagtag	gggtagcacc	cgctaaccgc	actcaaaaaa	4860
aaaagcaaac	aaacacacaa	attacggaca	caacaagttg	tttcaataag	ccatthttcca	4920
tagagcctaa	gtctaaatat	cgtagttata	ataatgggat	ccgcaacaaa	tcgagttgca	4980
acgaatgtta	agaacgctaa	cacaatacgc	atgtaaaatg	atactttaaa	attgatttag	5040
ttatttttagc	aacaatgaga	ttatctaaaa	ttgtttgatc	aaattttaca	ttctcgctat	5100
gtctatagat	aatttctaagc	ccgtaagccc	ataagcgtaa	tcgtaatcgt	aatcgtagcg	5160
tgtattttatg	ctcatatata	aacaactata	tatatatata	tatatatata	tatgtgcgga	5220
gtgcaacagt	gtctgtccag	taggagataa	gtctcgtttc	cgctcccctg	cttatgctat	5280
gaccttaggt	ccagggcaag	tatgagttac	cgaatctatc	tattaggtgc	atctaacgaa	5340
aggaatcatt	agctctgcac	gaactctagc	cgtagcctat	tgtaatccat	ttgtatgttt	5400
ggcttaagcg	ttttacttgt	tgaatataaa	gtgtaaaatt	atthtttgaaa	aaaaaaaacc	5460
cacacaaaac	acaaatcggt	tgttctatat	ttctgtttca	aaactaactc	gttaccacaca	5520
atccccctctg	ttatgtataa	ttaggatctc	tgtacac			5557

DAVI251.001APC\_sequence listing.TXT

<211> 1331

<212> PRT

<213> Drosophila

<400> 39

Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu  
1 5 10 15

Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His  
20 25 30

Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu  
35 40 45

Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser  
50 55 60

Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro  
65 70 75 80

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu  
85 90 95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser  
100 105 110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val  
115 120 125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His  
130 135 140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln  
145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile  
165 170 175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu  
180 185 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile  
195 200 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser  
210 215 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met

DAVI251.001APC\_sequence listing.TXT

225		230		235		240
Tyr	Asn	Gln	Ala	Gln	Lys	Met
		245		250		255
Asn	Asn	Asp	His	Gly	Gln	Ala
Val	Tyr					
Gln	Thr	Ser	Pro	Leu	Pro	Leu
		260		265		270
Asp	Ala	Ser	Val	Leu	His	Tyr
Ser	Gly					
Gly	Asn	Asp	Ser	Asn	Val	Ile
	275			280		285
Thr	Glu	Ala	Asp	Ile	Tyr	Glu
Asp						
His	Lys	Lys	His	Ala	Ala	Ala
	290			295		300
Ala	Ala	Ala	Ala	Ala	Ala	Gly
Gly	Gly	Gly	Ser			
Ile	Ile	Tyr	Thr	Thr	Ser	Asp
	305			310		315
Pro	Asn	Gly	Val	Asn	Val	Lys
Gln	Leu					
Pro	His	Leu	Thr	Val	Pro	Gln
		325		330		335
Lys	Leu	Asp	Pro	Asp	Leu	Tyr
Gln	Ala					
Asp	Lys	His	Ile	Asp	Leu	Ile
		340		345		350
Tyr	Ser	Thr	Thr	Asp	Gln	Lys
		355		360		365
Ser	Gly	Gly	Asp			
Ile	Gly	Ser	Leu	Val	Ser	Asp
	370			375		380
Gln	Val	Val	Val	Gln	Ala	Gly
Leu						
Pro	Tyr	Ala	Thr	Thr	Thr	Gly
				390		395
Gln	Pro	Val	Tyr	Ile	Val	
Ala	Asp	Gly	Ala	Leu	Pro	Ala
		405		410		415
Glu	Glu	His	Leu	Gln	Ser	Gly
Lys	Leu	Asn	Gly	Gln	Thr	Thr
		420		425		430
Pro	Ile	Asp	Val	Ser	Gly	Leu
Ser	Gln					
Asn	Glu	Ile	Gln	Gly	Phe	Leu
		435		440		445
Ser	Ser	Ser	Ala			
Thr	Val	Ser	Thr	Thr	Gly	Val
		450		455		460
Thr	Ile	Ser	His	His		
Gln	Gln	Gln	Gln	Gln	Gln	Gln
	465		470		475	480

DAVI251.001APC\_sequence\_listing.TXT

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala  
485 490 495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln  
500 505 510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg  
515 520 525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly  
530 535 540

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr  
545 550 555 560

Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser  
565 570 575

Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser  
580 585 590

Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr  
595 600 605

Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala  
610 615 620

Ser Gly Ala Gly Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly Gly  
625 630 635 640

Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr  
645 650 655

Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro  
660 665 670

Pro Pro Thr Ser Thr Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg  
675 680 685

Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr  
690 695 700

Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly  
705 710 715 720

Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala  
725 730 735



DAVI251.001APC\_sequence listing.TXT

Thr Thr Thr Val Leu Thr Ser Val His His His Gln Gln Gln Gln Gln  
740 745 750

Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Gln His His Gln  
755 760 765

Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr  
770 775 780

Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu  
785 790 795 800

Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp  
805 810 815

Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro  
820 825 830

Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser  
835 840 845

Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr  
850 855 860

Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp  
865 870 875 880

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys  
885 890 895

Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro Ile Ser  
900 905 910

Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly  
915 920 925

Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro  
930 935 940

Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu  
945 950 955 960

Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser  
965 970 975

Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn  
980 985 990

DAVI251.001APC\_sequence listing.TXT

Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn Ala Ile  
995 1000 1005

Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn Ile  
1010 1015 1020

Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly  
1025 1030 1035

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp  
1040 1045 1050

Thr Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys  
1055 1060 1065

Asp Lys Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala  
1070 1075 1080

Ala Lys Arg Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu  
1085 1090 1095

Leu Tyr His Pro Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln  
1100 1105 1110

Asp Phe Ala Lys Pro Pro Val Leu Phe Ser Pro Ala Glu Asp Met  
1115 1120 1125

Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr  
1130 1135 1140

Phe Asn Pro Leu Ser Asn Gly Asn Ser Asn Ser Asn Ser His Ser  
1145 1150 1155

Ser Leu Gln Ser Phe Tyr Gly His Glu Thr Asp Ser Pro Asp Leu  
1160 1165 1170

Lys Gly Ala Ser Pro Phe Leu Leu His Gly Gln Lys Val Ala Thr  
1175 1180 1185

Pro Thr Leu Lys Phe His Asn His Phe Pro Pro Asp Met Gln Thr  
1190 1195 1200

Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr  
1205 1210 1215

Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly Arg Met Thr

DAVI251.001APC\_sequence listing.TXT

1220																			
	Pro	Pro	Thr	Ser	Glu	Arg	Val	Met	Leu	Tyr	Val	Arg	Gln	Glu	Asn				
	1235						1240					1245							
	Glu	Glu	Val	Tyr	Thr	Pro	Leu	His	Val	Val	Pro	Pro	Thr	Thr	Ile				
	1250						1255					1260							
	Gly	Leu	Leu	Asn	Ala	Ile	Glu	Asn	Lys	Tyr	Lys	Ile	Ser	Thr	Thr				
	1265						1270					1275							
	Ser	Ile	Asn	Asn	Ile	Tyr	Arg	Thr	Asn	Lys	Lys	Gly	Ile	Thr	Ala				
	1280						1285					1290							
	Lys	Ile	Asp	Asp	Asp	Met	Ile	Ser	Phe	Tyr	Cys	Asn	Glu	Asp	Ile				
	1295						1300					1305							
	Phe	Leu	Leu	Glu	Val	Gln	Gln	Ile	Glu	Asp	Asp	Leu	Tyr	Asp	Val				
	1310						1315					1320							
	Thr	Leu	Thr	Glu	Leu	Pro	Asn	Gln											
	1325						1330												

<210> 40  
 <211> 18  
 <212> DNA  
 <213> murine

<400> 40  
 ggatcagaag accatgcc

18

<210> 41  
 <211> 18  
 <212> DNA  
 <213> murine

<400> 41  
 aggctgtag agttggtg

18

<210> 42  
 <211> 18  
 <212> DNA  
 <213> murine

<400> 42  
 ctgtagccag ctttcac

18

<210> 43  
 <211> 19  
 <212> DNA  
 <213> murine

DAVI251.001APC\_sequence listing.TXT

<400> 43	
gctggtgaaa aggacctct	19
<210> 44	
<211> 20	
<212> DNA	
<213> murine	
<400> 44	
cacaggacta gaacacctgc	20
<210> 45	
<211> 17	
<212> DNA	
<213> murine	
<400> 45	
cacattgaag aggtggc	17
<210> 46	
<211> 20	
<212> DNA	
<213> MURINE	
<400> 46	
aagggtgagc aggttcgctt	20